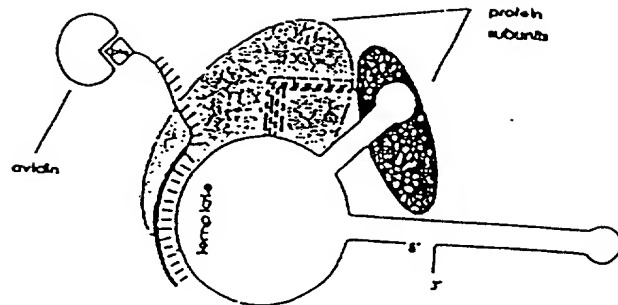


PANEL A



PANEL B

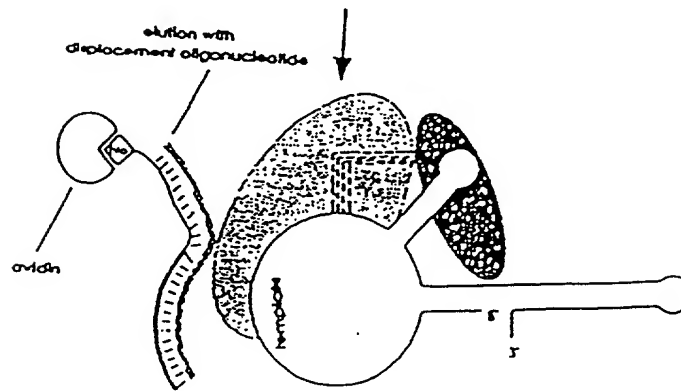


FIGURE 2

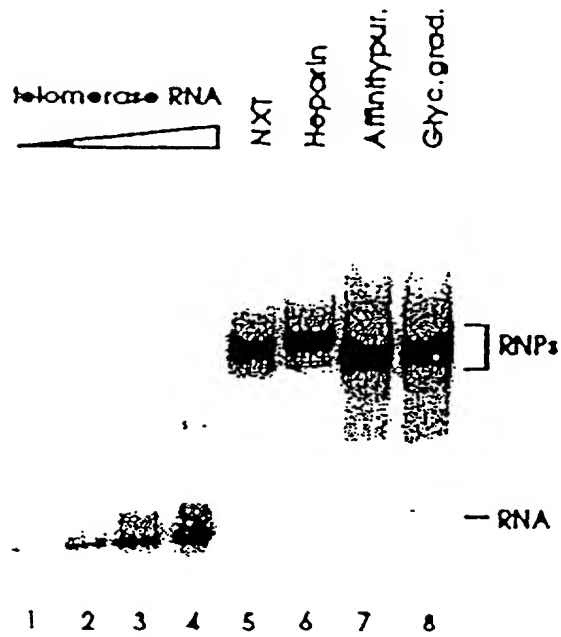


FIGURE 3

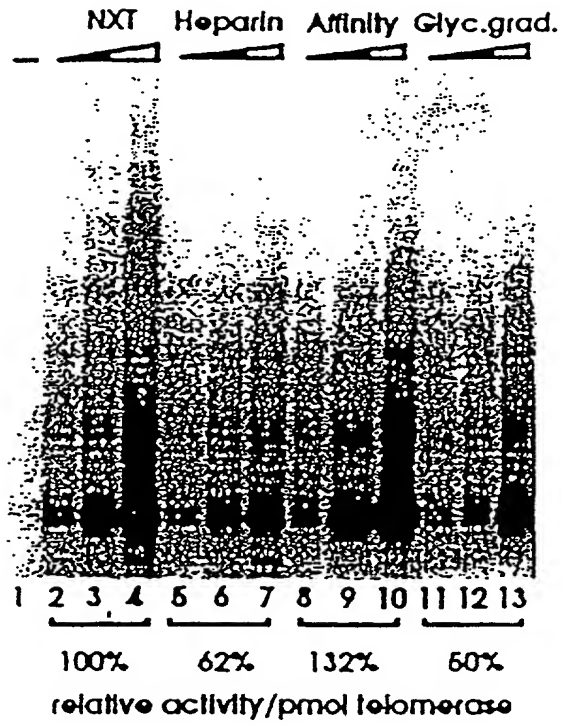


FIGURE 4

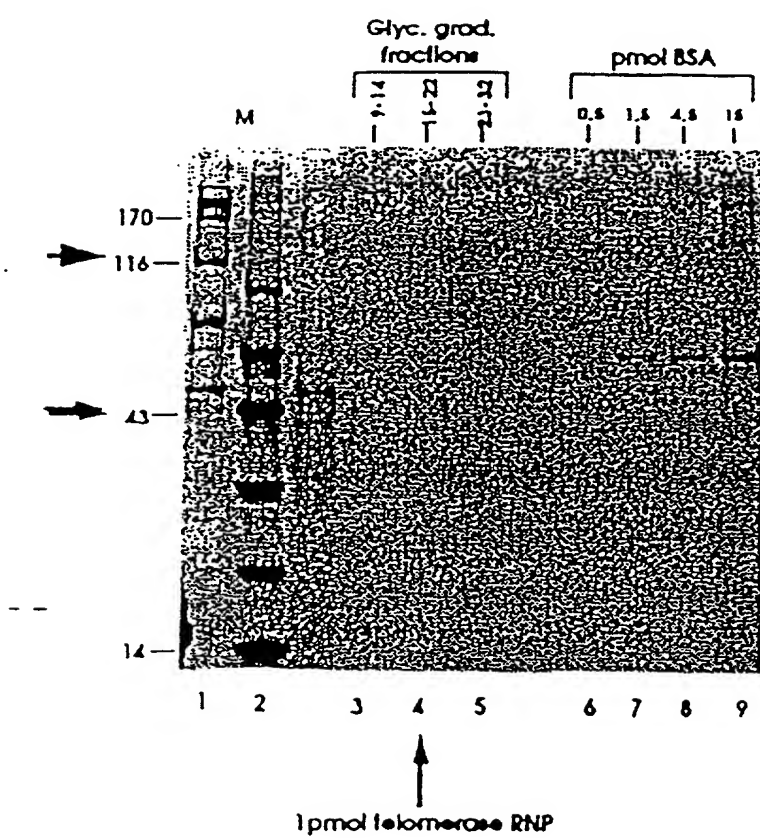


FIGURE 5

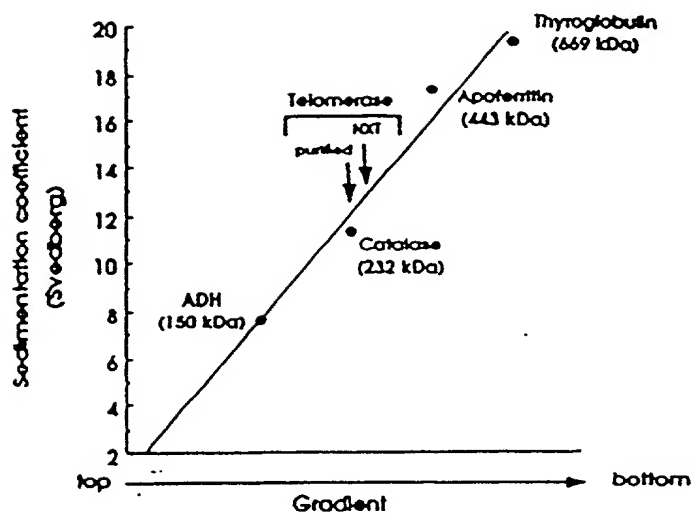


FIGURE 6

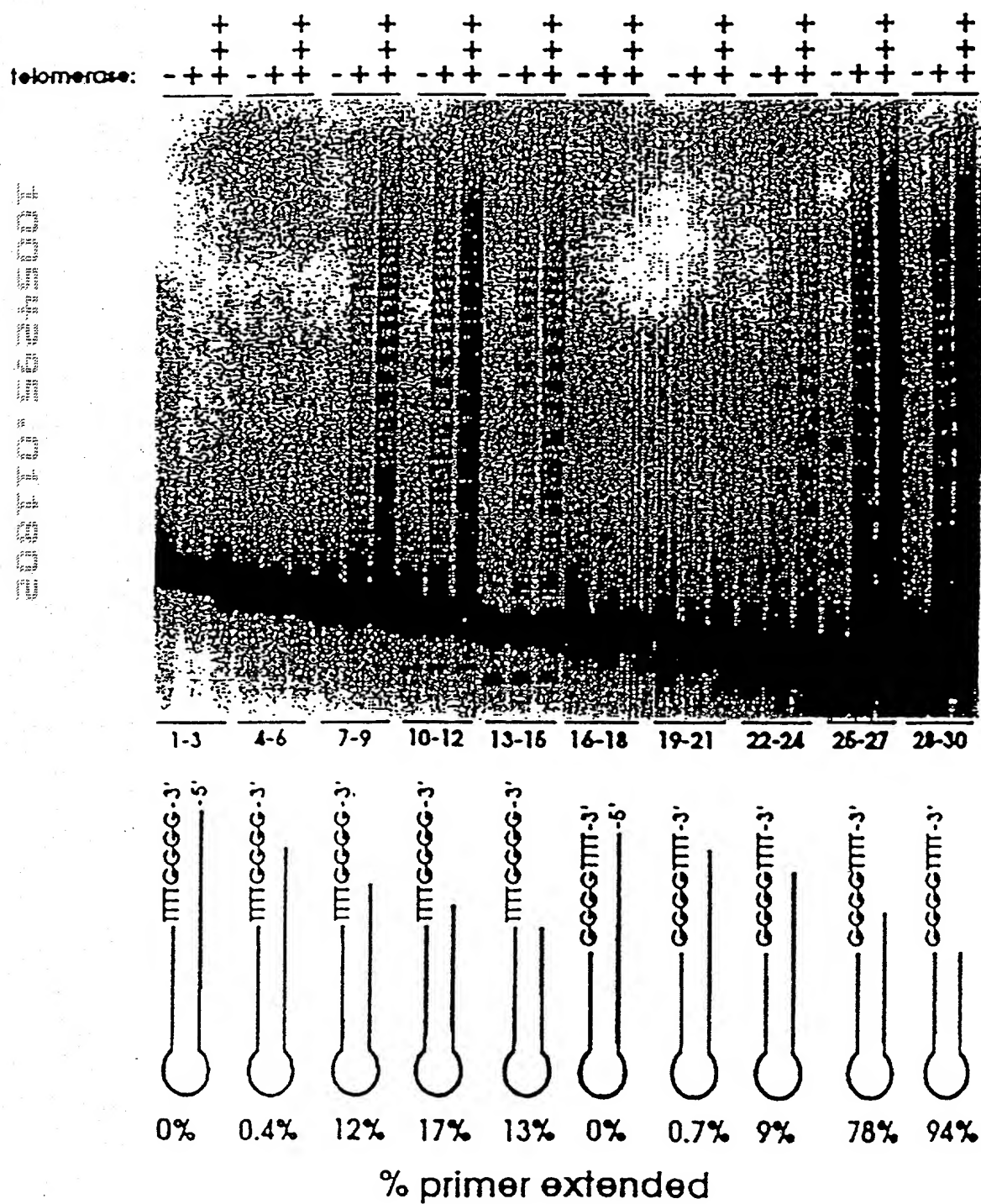


FIGURE 7

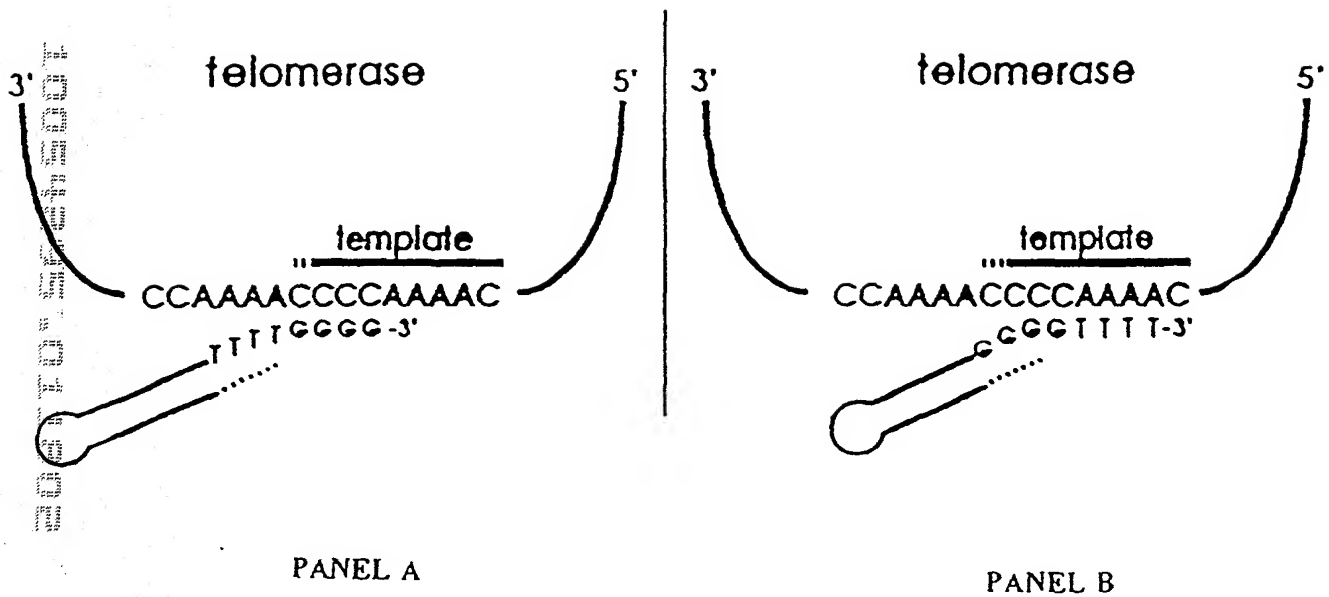


FIGURE 8

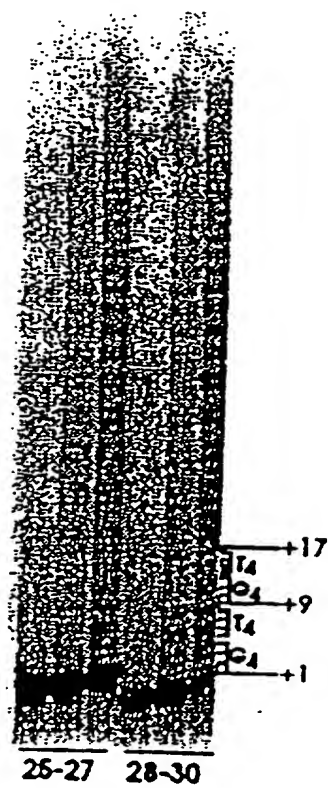


FIGURE 9

1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
 251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
 501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551 ATTGGAAATG AGCTCTTCGG ACATCTCTAC ACTAAATATT TAATATTCCA
 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTC
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
 1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
 1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACCTGA
 1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
 1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA
 1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
 1251 AAAAGAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTAC
 1301 AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
 1351 GGTTGAGACC TCTGCAAAGC ATTTTATTA TTTTGATCAC GAAAACATCT
 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
 1451 CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
 1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
 1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
 1651 ACCGAAGAAA ACTACTTTC GTCCAATTAT GACTTTCAAT AAGAAGATTG
 1701 TAAATTGAGA CCGGAAGACT ACAAATTA CTACAAATAC GAAGTTATTG
 1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
 1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
 1851 AGTTTGTGTTG CAAATGGAAG CAAGTTGGAC AACCAAACT CTTCTTTGCA
 1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC
 1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
 2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
 2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
 2101 TGCATTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTGAAAATG
 2151 AACAAAATGA CTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
 2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
 2251 CCAATATAAT TACATTAAT TTAATGGGAA GTTTTATAAA CAAACAAAAG
 2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTATC ATTTTATTAT

FIGURE 9 (cont.)

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651 TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACTCT
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201 CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTGG TCTTATATAC
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

FIGURE 10

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
 51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
 101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
 151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
 201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNMKSRTTR IFYCTHFNRN
 251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNIRKKLK DKVIEKIAM
 301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
 351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHელი
 401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS
 451 LIRCFYVTE QQKSYSKTY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
 501 EEWKKS LGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
 551 NSHMLKTLK NRMFKDPFGF AVFNYYDDVMK KYEEFVCKWK QVGQPKLFFA
 601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVDSKN
 651 FRKKEMKD YF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKT LIVEAKQ
 701 RNYFKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
 751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVL FIEKL
 801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
 851 SIDMKTALM PNINLRIEGLCTLNLNMQT KKASMWLKKK LKSFLMNNIT
 901 HYFRKTTITTE DFANKTLNKL FISGGYKYM CAKEYKDHFK KNLAMSSMID
 951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
 1001 KYIFNRVCM I LKAKEAKLKS DQCQSLIQYD A

FIGURE 11

1 CCCCCAAACC CCAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG
 51 GTAGTTTGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
 101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
 151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
 201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
 251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
 301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
 351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
 401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTT
 451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
 501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
 551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG
 601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
 651 TTGAGACAAT TGAAAAAGCT GTTTACAAC GAAGGAATCG CAGTTCTGAA
 701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
 751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
 801 TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
 851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
 901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
 951 AAAAGAAGCA GCGGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
 1001 TTGTTGATTG TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
 1051 AAAGAAGAAG AGCTATCACA ATCCTGATTG TTAAAGATTT CAAAAATTCC
 1101 AGGTAAGAGA GATACATTCA TTAATAATTCA TATATTATAG TTTTTCATT
 1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
 1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
 1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
 1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
 1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
 1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
 1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA
 1501 GTAACCTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
 1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
 1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
 1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
 1701 AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
 1751 GGGGTTTTGG GG

FIGURE 12

1 CCCCCAAACCCCAAAACCCCAAAACCCCTATAAAAAAGAAAAATTGAGGTAGTTTAGA
 ----- 60
 GGGGTTTGGGGTTTGGGGTTTGGGGATATTTTTCCTTTTAACTCCATCAAATCT

 a P Q N P K T P K P L * K K K K L R * F R -
 b P K T P K P Q N P Y K K R K N C G S L E -
 c P K P Q N P K T P I K K E K I E V V * K -

 AATAAAATATTATTCCTCCGACAAATGGAGATGGATATTGATTGGATGATATAGAAAATT
 61 ----- 120
 TTATTTTATAATAAGGGCGTTTACCTCTACCTATAACTAAACCTACTATATCTTTAA

 a N K I L F P H K W R W I L I W M I * K I -
 b I K Y Y S R T N G D G Y C F G C * Y R K F -
 c * N I I P A Q M E M D I D L D D I E N L -

 TACTTCTAATACATTCAACAAGTATAGCAGCTCTGTAGTGACAAGAAAGGATGCAAAA
 121 ----- 180
 ATGAAGGATTATGTAAGTTGTTTCATATCGTCGAGAATCACTGTTCTTCTACGTTT

 a Y F L I H S T S I A A L V V T R K D A K -
 b T S * Y I Q Q V * Q L L * * Q E R M Q N -
 c L P N T F N K Y S S S C S D K K G C K T -

 CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
 181 ----- 240
 GTAACCTTAGACCGAGCTTAGCGGAAGTAAGTTGATAAGGTTTCAACGTTTTTGTTAATC

 a H C N L A R N R L H C L F Q S C K N N * -
 b I E I W L E I A F I D Y S K V A K T I R -
 c L K S G S K S P S L T I P K L Q K Q L E -

 AGTTCTACTTCTCGGATGCAAAATCTTTATAACGATTCTTCTTGAGAAAATTAGTTTAA
 241 ----- 300
 TCAAGATGAAGACCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTAATCAAAATT

 a S S T S R M Q I F I T I L S C E N * F * -
 b V L L L G C K S L * R F F L E K I S F K -
 c F Y F S D A N L Y N D S F L R K L V L K -

 AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
 301 ----- 360
 TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

 a K A E S K E * K L K H Y * C L N K I R * -
 b K R R A K S R N C N I T N V * I K S G N -
 c S G E Q R V E I E T L L M F K * N Q V M -

 TGAGGATTATTCTATTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
 361 ----- 420
 ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCTCGTAATACCTCTTTTAATGAATT

 a C G L F Y F L D H F L R S I M E K I T * -
 b E D Y S I F * I T S * G A L W R K L L N -
 c R I I L F F R S L L K E H Y G E N Y L I -

 TACTAAAGGTAACAGTTTGGATTATTTCCCTAGCCAACATGATGAGTATATTAATT
 421 ----- 480
 ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTACTACTCATATAATTAA

 a Y * K V N S L D Y F P S Q Q C C V Y * I -
 b T K R * T V W I I S L A N N D E Y I K F -
 c L K G K Q F G L F P * P T H M S I L N S -

FIGURE 12 (cont.)

481 CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT 540
GTATACTCTTACTCAGTTTCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

a H H R M S Q R I S I H Q T Y Q R Q T R Y -
b I C E C V K G S R Y I R L T K D K L A I -
c Y E N E S K D L D T S D L P K T N S L -

541 AAAACCGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATGCAATTTACTATTTCG 600
TTTTGCGTTCTTTTCAAACATTAGCTTGTCTCTTCTGAATAACGTAATGATAAGC

a K T Q E K V C * S N S R R T Y C I Y Y S -
b K R K K K F D N R T A E E L I A F T I R -
c N A R K S L I I E Q Q K N L L H L L F V -

601 TATGGGTTTTATTACAATGTTTTAGGTATCGACGGTGAACCTCCCGAGTCTTGAGACAAT 660
ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

a Y G F Y Y N C F R Y R R C T P E S C D N -
b M G F I T I V L G I D G E L P S L E T I -
c W V L L Q L F * V S T V N S R V L R Q L -

661 TGAAAAAGCTGTTTACAACCTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT 720
ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

a C K S C L Q L K E S Q F C K F * C V C H -
b E K A V Y N C R N R S S E S S D V Y A I -
c K K L F T T E G I A V L K V L M C M P L -

721 TATTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA 780
ATAAAACACTTAATTAGAGTTTATAGAAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a Y F V N * S Q I S Y L N L M D S Y R N K -
b I L C I N L K Y L I S I * W I A I E T N -
c F C E L I S N I L S Q F N G * L * K Q T -

781 CCAAATAAACCATGCAAGTTTAAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC 840
GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCTGTTTACGTGTG

a P N K P C K F N G I Y V K S F G T N A H -
b Q I N H A S L M E Y T L N P L G Q M H T -
c K * T Y Q V * W N I R * I L W D K C T L -

841 TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC 900
ACTTAAATATAACCTAAGAATTTCTGATCTATGTGTCTTACGAAATCTCTGACTAAATCG

a C I Y I G F L K H R Y T E C F R D C F S -
b E F I L D S * S I D T Q N A L E T D L A -
c N L Y * I L K A * I H R M L * R L I * L -

901 TTACAACAGATTACCTGTTTGGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA 960
AATGTTGCTTAATGGACAAAACCTAATGAGAACGAGTAGAGAATATAGAAATTTCTTCGT

a L Q Q I T C F D Y S C S S L I S L K E A -
b Y N R L P V E I T L A H L L Y L * K K Q -
c T T D Y L F C L L L I S Y I F K R S R -

961 GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC 1020
CCGCTTACTTTTCTTCTGATTCTTTCTCTAAAGTTTAAACAACCTAAGAAGACATTGG

a G E M K R R L K K E I S K F V D S S V T -
b A K C K E D * R K R F Q N L L I L L * P -
c R N E K K T K E R D F K I C C F F C N R -

1021 GGAATTAACAACAAGAAATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTC 1080
CCTTAATGTTGTTCTTAATCGTTGCTTTTCTTCTCTCGATAGTGTAGGACTAAG

a G I N H X N : S N E K E E E L S Q S C F -
b E L T T R I L A T K K K K S Y H N P D S -
c N * Q Q E Y * Q P K R R R A I T I L I L -

FIGURE 12 (cont.)

1081 TTAAGATTTCAAAAATCCAGGTAAGAGAGATACATTCAAAAATTCATATATTATAG 1140
AATTTCTAAAGTTTAAAGGTCCATTCTCTCTATGTAAGTAATTTAAGTATATAATATC

a L K I S K I P G K R D T F I K I H I L -
b * R F Q K F Q V R E I H S L K F I Y Y S -
c K D F K N S R * E R Y I H * N S Y I I V -

1141 TTTTTCATTTCACAGCTGTTATTTCTTTTATCTTAACAATATTTTGTAGCTGGAA 1200
AAAAAGTAAAGTGTGACAATAAAGAAATAGAATTGTTATAAAAACTAATCGACCTT

a F F I S Q L L F S F I L T I F F D * L E -
b F S F H S C Y F L L S * Q Y F L I S W K -
c F H F T A V I F F Y L N N I F C L A G S -

1201 GTAAAAAGTATCAATAAGAGAAGCGCTAGACTGAGGTAACCTAGCTTATTCACATTCAT 1260
CATTTTTCATAGTTTATCTCTCTCGCGATCTGACTCCATTGAATCGAATAAGTGAAGTA

a V K S I K * E K R * T E V T * L I H I H -
b * K V S N K R S A R L R * L S L F T F I -
c K K Y Q I R E A L D C G N L A Y S H S -

1261 AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA 1320
TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTTT

a R S T F I Y P I R C * G N S S H P F * K -
b D R P S Y I Q Y D D K E T A V I R F K N -
c I D L H I S N T M I R K Q Q S S V L K I -

1321 TAGTGCTATGAGGACTAAATTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA 1380
ATCAGGATACTCCTGATTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

a * C Y E D * I F R V K K W S R N L N O K -
b S A H R T K F L E S R N G A E I L I K K -
c V L C G L N F * S Q E H E P K S * S K R -

1381 GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTGTTAATAAGTATTACCA 1440
CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTAGAAAGCAATTATTCATAATGGT

a E L R R Y C K R I E L * I F R * * V L P -
b N C V D I A K E S N S K S F V N K Y Y Q -
c I A S I L Q K N R T L N L S L I S I T N -

1441 ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAGAAATAAA 1500
TAGAACTAACTTCTCTAACTGCTCCGTTGACGTCTTCTAGTAATTTCTTTATTT

a I L I D C R D * R G N C T E D H * R N X -
b S C L I E E I D E A T A Q K I I K E I K -
c L D C L E K R L T R Q L H R R S L K K * S -

1501 GTAACCTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA 1560
CATTGAAAATAATTAATCTCTTATTTGATTAAATGATTATATCTCTAGTCGCTAGAAGTT

a V T F I N * R I N * I T N I E I S D L Q -
b * L L L I R E * T K L L I * R S A I F N -
c N F Y * L E N K L N Y * Y R D Q R S S I -

1561 TTGACGAATAAAGCTGAACATAAGTTAGACAATAAAAAATACAAACCTTGCTCAAAAT 1620
AATGCTTTATTTTCGACTTGATTCAATCTGTTATTTTATGTTTGAACCAAGTTT

a L T K * K L N * S * T I K N T N L C Q N -
b C R N K S C T K V R Q * K I Q T L V K I -
c D E I K A E L K L D N K K Y K P W S K Y -

1621 ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAATAAGGCAATAAATAAATGA 1680
TAACTCCTTCCTTTCTCTCGTCAATCGTTTTCTTTTATTCGTTATTTATTTTACT

a I E E G K E D Q L A K E K I R Q * I K C -
b L R K E K K T S * Q K K K * G N K * N E -
c C G R K R R P V S K R X N K A I N K H S -

FIGURE 12 (cont.)

1681 GTACAGAAGTGAAGAAATAAAAGATTATTATTTTCAATAATTTATTGAAAAGAGGGGTT 1740

CATGTCTTCACTTCTTTATTCTAAATAAAAAAGTTATTAAATAACTTTTCTCCCAA

a	V	Q	K	C	R	N	K	R	F	I	F	F	N	N	L	L	K	R	G	V	-
b	Y	R	S	E	E	I	K	D	L	F	F	S	I	I	Y	C	K	E	G	F	-
c	T	E	V	X	K	*	K	I	Y	F	F	Q	*	F	I	E	K	R	G	F	-

1741 TTGGGGTTTTGGGGTTTTGGGG 1762

AACCCCAAAACCCCAAAACCCC

a	L	G	F	W	G	F	G	-
b	W	G	F	G	V	L	G	-
c	G	V	L	G	F	W	-	

FIGURE 13

2 EVDVNOADNHGIHSALKTCCEEIKEAKTLYSWIQKVICRNOQSQSHYKDL 51
 19 ELEEEMQENQNDIQVRVK...IDDPKQY...LVNVTAACLLQEGSYQDK 62
 52 EDIKFAOTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL 100
 63 DERRVITKALL...EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF. 107
 101 SSSDVSORQKLQCFGFQKGNQLAKTHLLTALSTQKQYFFQDEWNOVRAM 150
 108 CVVHKNTQPFIEKYFNKAVLLPNDLLEVECEFAQVLYI 144
 151 IGNEFRHLYTKYLIFORTSEGLVQFCGNNVFDHLKVNDFDKKQKGG 200
 145 FDATEFKNLY...LDRILSQDIRKELTFRKCLQRCVRSKF 181
 201 ADMNE PRCCSTCKYNVKNKDHFLNNINVPNNNNMKSRTIFCYCTHF 247
 182 SEFNEYOLGKYCTES...QRKKTMFYRLSVTNKQKWDQTKKK... 220
 248 NRRNQFFKKHEFVSNNKNNISAMDRAQTIFTNIFRNRIRKKLKDVKIEKI 297
 221 RKENLLTKLQAIKESEDKSKRETG...DIMNVEDAIAKALPAVMKKI 264
 298 AYHLEKVKDFNFNYLTSCPLPENWRERKQKIENLINKTREEKSKYYEE 347
 265 AKRQNAHK...KHMKA PKIPNSTLESXYLTFRD 294
 348 LFSYTTDNKCVTFINEFFYNILPKDFLTGRNRKNFQKVKKYVELNKHE 397
 295 LIKFCHISEP...KERVYKILGKKYPKTEEEYKAAPGDSASAPFN.PE 338
 398 LIHKWLLLEKINTREISWQVETSAKHFYFDHENIYVLWKLRLWIFEDL 447
 339 LACKRMKIEISKTWENELSAKNTAEVWNLISSNQLPYMAMLRNLSN... 386
 448 VVSLIRCFYVTEOQKSYSKTYYYRKNWVIMKMSIADLKKETLAEVQE 497
 387...ILKAGVSD... 394
 498 KEVEEWKKS LGFAPGKLRLIPKKTFRPIMTFNKKIVNSDRKTTKLTNT 547
 395...TTHS 398
 548 KLLNSHMLKTLKNRMFKDPFGFAVFNYYDDVMKKYEEFVCKWKQVQPKL 597
 399 IVINK...ICEPKAVENSKM 415
 598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNIVID 647
 416 F...PLOFFSAIEAVN.EAVTKGFKAKK...RENNMLKGQIEAVKE...VVE 457
 648 SKNFRKKEMKDYFRQKFKIALEGGQYPTLFSVLENEQNDLNAKKT LIVE 697
 458 KIDEKKDM...ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496
 698 AKQRNYFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS 747
 497 IAVNNLDEIKGHTAIFSDVSGSMSTSMGGAKKYGSVRTCLECALVLGL 546
 748 FYYATLEESSLGFLRDESMNPENPNVLLMRLTDDYLLITTQENNAVLFI 797
 547 MVKQRCESSEFYIFSSPSSQCNKCYLEVDL... 576
 798 EKLINVSRENGFKFMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
 577...PGDEL RPSMQKLLQEKGLGGG...TDFPYECIDEWTKNKT HVD 617
 847 WIGISIDMXTLALMPNINLRIGILCTLNLMQTKKASMWLKKKLSFLM 896
 618 NIVILSDMMIAEGYS DINVRGSSIVNSI...KKYKDEVN 653
 897 NNITHYFRKTITTEDFANKTLNKLFISSGGYKYMOCACEYKD.HFKKNLAM 945
 654 PNKIF...AVDLEGY...KCLNLGDEFNENNYIKIFGM 687
 946 SSMIDLEVSKIIYSVTRAFFKYLVCNKOTIFGEEHYPDFFLSTLKHFI 995
 688 SDSI...LKFISAKQGA...MMVE 706
 996 IFSTKKYIFNRVC 1008
 707 VI...KNFALQKIG 717

FIGURE 14

132 LSTQKQYFFQDEWNOVRAMIGNEL.FRHLYTKYLIFORTSE..GTLVQFC 178
 1 MSRRNQ...KKQAPIGNETNLDVFLQNLLEVYKSQIEHYKTOQQOI 43
 179 GNNVFDHLKVNDKFDKKQKGAADMNEPRCCSTCKYNVQNEKDHFLNNIN 228
 44 KEEDLKLLKFKNQDQDGNNGDDDEE.....NNSNKQQLRRVN 84
 229 VPNWNNHKSRTIRIFYCTHFNRRNQFFKKHEFVSNNKNISAMDRAQTIFTN 278
 85QIKQVQLIKK...VGSKEKDLNLNEDENKKN 114
 279 IFRFNRIKKLKDVKIEKIAYMLEKVDFNFNYLTSCPLPENWRERKQ 328
 115 GLSEQVKEEQRLTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY 164
 329 KIENLINKTREESKYEEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
 165 DTEKWFESHQK.....NYVSIYANQKTSYCWMLKDYFNK 200
 378 RNRKNFQKKVKKYVELNKHLEIHNLLLEKINTREISWMQVETSAKHFFY 427
 201 NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID..... 242
 428 FDHENIYVLWKLRLWI..FEDLVVSLIRCFFVTEQQKSYSKTYYYRKN 475
 243 VNFNNLCILALLRFLLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290
 476 WDVIMKMSIADLKKETLAEVQEKEVEEWKSLGFAPGKLRLIPKKTFRP 525
 291 FAVVFSHR..HLQGIHLQVPCFAFYLVNSSSQISVKDSQLQ 330
 526 IMTFNKKIWNDRKTTKLTNTKLLNSHMLKTLKNRMFKDPFGFAVFN 575
 331 VYSFSTDLKLVD..TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL 378
 576 DDVHKYEEFVCKWKQVQPKLF.....FATHDIEKCYDS..VNREK 615
 379 NVLLKKVKH..ANLNLVSIPTQFNDFYFVNQLHLKLEFGLPNILTKQK 426
 516 LSTFL KTTKLLSSDFWIMTAQILKRNNI..VIDSKNFRKKEMK 657
 427 LENLLLSIKOSKNLKLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNO 476
 558 DYFRQKFQKIALEGGOYPTLFSVLEN EQNDLNAKKTLLIVEAKQRYNFK 705
 477 EETPETKDETPSESTSGMKFFDHLSELTELEDFSVN..LQATQEIY 520
 706 KDNELQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYATLEE 755
 521 DSLHKLIRSTNLKKFKLSYKYEKSKMDTFIDLKNI.....YETLNN 564
 756 SSLGFLRDESNPENPNVNLMLRLTDDYLLITTQENNAVLFIKLINVSR 905
 565 ..LKRCVWISNPHGNISYELTN.....KDSTFYKFKLTNQE 500
 806 ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK 855
 501 LQHAKYTFK..QNEFOFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ 648
 856 TLALMPNINLRIEGILCTLNLMQT..KKASHWLKK..KLKSFLMNNITH 901
 649 NVNI..IASLLYPNNIQKNPKNPKNLLFFKQFEQLKNLENVSINC 691
 902 YFRKTI..TTEDFANKTLNKLFISSGYKYMCAKEYKDHFKKNLAMSSM 948
 692 ILDOHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFTLQQLPEL 741
 949 IDLEVSKIIYSVT.....RAFFKYLVCNIKDT..IFGEEHY 982
 742 NQVYINQOLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSTLQQLIDF 791
 983 PDFFLS TLNHFIEIFSTKKY IFNRVCHILKAKEAKLKSQDQOSLIQ 1028
 792 DQNTVSODSISIKNILESISESKYHHYLRNPSQSSSLIKSENEEQELLK 840

FIGURE 15

[illegible]

```

1  MEMDIDLDDIENL. . . . LPNTFNKYSSSCDDKKGCKTLKSGSKSPS. . . 42
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
491 IELAIKIAVNNKLDEIKGHTAIFSDVSGSMSTSHSGGAKKYGSVRTCLEC 540
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
43  LTIPKLQKO. . . . LEFYFDANLYNDSFLRKLVLKSGEORVEIETLL 85
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
541 ALVLGLMLVKORCEKSSFIYSSPSSQCNCYL. EVDLPGLDELPSHQKLL 589

```

FIGURE 17

	Motif A	Motif B
Consensus	h--h <h>h</h> h--h--h	h----+-- <h>h</h> h--h--h
telomerase p123	GQFKLFFATMDIEKCYDSVNRKLSFLKTYTKLL-100-RFYKQTKGIF <h>h</h> CLCVSSILSSFYATLEZSSSLGFL	
Dong (LINE)	KNRNLHCTYIDYKKAFDSIPHSLVLIQVLEIYKIN-28-RQLAIKGIY <h>h</h> CDLSL <h>h</h> WFCALNPLSHQLHNDR	
al S.c. (group II)	FGGSNWFRVLDLKKCFDTISHDLIIKELKRYISD-26-HVPVGPRVCV <h>h</h> CAPTSPALCNAVLLRLDRRLAGLA	
HIV-RT	LKGGKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP-7-GIRYQYNVLF <h>h</h> GWKGS <h>h</h> PAIFQSSMTKILEPFRKQN	
L8543.12	VLPELYFMKFLVKSCTDSIPRMECMRILKDALKN-68-KCYIREOGLE <h>h</h> CESSLSA <h>h</h> IVDLVYDDLLLEFYSEPK	

	Motif C	Motif D	Motif E
Consensus	h--Y <h>h</h> DD <h>h</h> h	<h>h</h> h-h--h-- <h>h</h>	h-h <h>h</h> h-h
telomerase p123	-14-LMRLLTDDYLLITTTQENN-0-AVLFIKLLINVSREN <h>h</h> FKFN <h>h</h> RLQT-23-QDYCDWIGISL		
Dong (LINE)	-16-HLIYMDIILYAKNDKE-0-MKKLIDTTTIFSNDSMQFGLRCKT-25-KCJYKYLGFFQQ		
al S.c. (group II)	-55-YVRYADDILIGVLSKN-2-KIIRDLNNFLNS <h>h</h> GLTINEERTLI-4-ETPARFLGNYI		
HIV-RT	-4-IYQYMDLLYVGSHLEIG-1-HRTKIEELRQHLRLWGLTTPDRKHQK-0-EPFLWMGYEL		
L8543.12	-8-ILKLLADDFLIISTDQQQ.....VINIKKLAMC <h>h</h> QKYNAR-41-IRSKSSKGI		

FIGURE 18

telomerase p43	LQKQIEEYFSDANLYNDSFLRKLVLKSGEQRVEIETLLM
human La	ICHQIEEYFSGDENLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA	ICEQIEEYFSGDENLPRDKFLKQOI.LLDDGWVPLETMIK
Drosophila La	ILROMEYFEGDANLNRDKFLREQIGKNEDGWVPLSVLVT
S. c. Lhplp	CLKOMEYFSEFNFPYDRELRTTAEK.NDGWVPISTIAT

FIGURE 19

1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
 61 tagatttaatt ttgaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
 181 tatataagtt aggggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcaactgcagc
 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
 301 taaagcactt ctgaggttg ctgagtcga tcctgagttc atctgctagt tggcagtcta
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat ttgtgtgt
 421 ccacaagaat actcaacctt tcatcgaaaa gtacttcaac aaagcagtac ttitgcctaa
 481 tgacttactg gaagtcgtgt aatttgata ggttctctat attttgatg caactgaatt
 541 caaaaatttg tatcttgata ggatacttc ataagatatt cgtaaggaaac tcactttccg
 601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
 781 ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
 841 agatgcaatc aaggctttta aaccagcagt tatgaagaaa atagccaaga gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaaat tcttaactct accttgaat caaagtactt
 961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
 1021 gatecttggg aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
 1081 tgcacttgca ccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
 1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaatt
 1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
 1261 cgggtgttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
 1321 tgagaactcc aagatgttcc ctctcaatt ctttagtgcc attgaagctg ttaatgaagc
 1381 agttactaag ggattcaagg ccaagaagag agaaaatag aatcttaaag gtcaaatcga
 1441 agcagtaag gaagtgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
 1501 aaccgaagaa ggagaatttg taaagtcaa cgaaggaatt ggcaagcaat acattaaactc
 1561 cattgaactt gcaatcaaga tagcagttta caagaattta gatgaaatca-aaggacacac
 1621 tgcaatcttc tctgatgttt ctggttctat gaggacctca atgtcaggtg gagccaagaa
 1681 gtatggttcc gttcgtactt gtcctgagtg tgcattagtc ctggtttga tggtaaaata
 1741 acgtttgaa aagtctcat tctacatctt cagttcacct agttctcaat gcaataagtg
 1801 ttacttaaga gtgatctcc ctggagacga actccgtcct tctatgtaaa aacttttgca
 1861 agagaaagga aaacttgggt gtggtactga ttcccctat gaggcattg atgaatggac
 1921 aaagaataaa actcacgtag acaatatcgt tatttgtct gatatgatga ttgcagaagg
 1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
 2041 tgaagtaaat cctaacatta aaactttgc agttgactta gaaggttacg gaaagtgcct
 2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggtta tgagcgattc
 2161 aatcttaag ttacttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
 2221 ctttgcctt caaaaaatag gacaaaagt agtttctga gattcttcta taacaaaaat
 2281 ctcacccac tttttgtt tattgcatag ccattatgaa atttaaat taatctattt
 2341 atttaagtt cttacatagt ttatgtatcg cagttctta gcctattcaa atgattctgc
 2401 aaagaacaaa aaagattaaa a

FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN
YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS
QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMTFRYLSVTNKQKWDQTK
KKRKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK
APKIPNSTLESKYLTTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFSGDSASAP
FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV
SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNLKGQIE
AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG
HTAIFSDVSGSMSTSMSSGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ
CNKCYLEVDPGDELSPSMQKLLQEKGLGGGTDFFPYECIDEWTKNKTHTVDNIVILSD
MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKJFAVDLEGYKCLNLGDEFNENNYI
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

FIGURE 21

1 tcaatactat taattaataa ataaaaaaaa gcaactaca aagaaatgt caaggcgtaa
 61 ctaaaaaag ccataggctc ctataggcaa tgaacaaat ctgattttg tattacaaa
 121 tctagaagt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
 181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
 241 tgaatgatga gaagaaaaca actcaataa ataataagaa ttattaagga gagtcaatta
 301 gattaagtag caagttaat tgataaaaa agttgggtct aaggtagaga aagatttgaa
 361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
 421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtatta acatggacta
 481 ccagttagat ttaaatgaga gtgggtggcca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaat tatgtatcaa ttacgcca
 601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaa attatgatca
 661 tcttaatga agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt
 721 ttcaaaaaca atcaaaactta ctaataattc ttactagact gtaacatag acgttaattt
 781 tgataataat ctctgtatc tcgattgct tagattttta ttactactag aaagattcaa
 841 tattttgaat ataagatctt ctatacaag aaattaatat aattttgaga aaattggtga
 901 gctactgaa actatcttcg cagttgtctt ttctatcgc cactacaag gcattcattt
 961 acaagttcct tgcgaagcgt tctaatttt agttaactcc tcatcataa ttacggttaa
 1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaaca
 1081 agtccaagat tattttaagt tcttataaga attccctcgt ttgactcatg taagctagta
 1141 ggctatccca gttagtgtca ctaacgctgt agagaacctc aatgtttac ttaaaaaggt
 1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt
 1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca
 1321 aaagcttgaa aatctacttt tgagtataaa ataatacaaa aatcttaaat ttttaagatt
 1381 aaacttttac acctacgttg ctaagaaac cccagaaaa cagatattaa aacaagctac
 1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa cttaaagatga
 1501 aactccaagc gaaagcaca gtggtatgaa atttttgat catctttctg aattaaccga
 1561 gctgaagat ttacgctgta acttgtaagc tacccaagaa attatgata gcttgacaa
 1621 acttttgatt agatcaaca atttaaagaa gttcaatta agttacaaat atgaatgga
 1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
 1741 taaaagatgc tctgttaata tatcaaatcc tcatggaac atttctatg aactgacaaa
 1801 taaagattct actttttata aatttaagct gaccitaaac taagaattat aacacgctaa
 1861 gtatctttt aagtagaacg aattttaatt taataacgtt aaaagtcaa aaattgaatc
 1921 ttcccaata gaaagcttag aagatattga tagtctttgc aaatctattg ctcttgtaa
 1981 aaattacaa aatgttaata ttatcgccag ttgtctctat ccaacaata tttagaaaa
 2041 tctttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaatttga
 2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt
 2161 agaaaagaat aaaaaataa aagcattcat ttgaaaaga tattatttat tacaatatta
 2221 tcttgattat actaaattat taaaacact tcaatagttt cctgaattaa attagttta
 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaagaat catcctaacc
 2401 ccttagtcta atagattttg accaaaacac tgaagtgtat gactctatta aaaagatttt
 2461 agaatttata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag
 2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa
 2581 aggtgtttta gtaaagcat actataaatt cctctatgt ttaccaactg gtacttatta
 2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaataaaa tattaataat
 2701 tgaatatttc ttgcttatt attgaataa tacatacaat agtcatttt agtgtttga
 2761 atatatttta gttatttaatt tcatattttt aagtaataa ttattttica atcattttt
 2821 aaaaaatcg

FIGURE 22

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQKIK

EEDLKLLKFKNQDQDGNNGNDDDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK

DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR

ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNDHNLNVSINRLETEAE

FYAFDDFSQTIKLTNNSYQTVNIDVNFDDNLCILALLRFLSLERFNILNIRSSYTRN

QYNFEKIGELLETIFAVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF

STDCLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL

VS IPTQFNFDYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY

VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED

FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK

RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKS AKIE

SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNNLFFKQFEQLK

NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFKTLQQLPE

LNQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFDQNTVSD

DSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP

LCLPTGTYDYNSDRW

FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL
PNSRKIALPCLPGDLSHKAVIDHCHYLLTGELYNNVLTFGYKIARNEDVNNSLFCHS
ANVNVTLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK
WVQRSSSSSATAAQIKQLTEPVTNKQFLHKLNNSSSFFPYSKILPSSSSIKKLTDLR
EAIFPTNLVKIPQRLKVRJNLTLQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLR
QSPKERVLFIIIVILQKLLPQEMFGSKKNKGKIIKNLNLNLLSLPLNGYLPFDSLLKKL
RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLFRLIPKIIQTFFYCTEISSTVTI
VYFRHDTWKNLITPFIVEYFKTYLVENNVCRNHNSYTLNHNHSMRIIPKKSNEFR
IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE
FKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN
TNTGVLKLFNVVNASRVKPYELYIDNVRTVHLSNQDVINVVEMEIFTALWVEDKCY
IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV
INIKKLAMGGFQKYNANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN
NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF
KDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIEYEVRFILNGFLESLSNTS
KFKDNIILLRKEIQHLQAYIYIYIHVN

Figure 6

Oxytricha
Euplotes

LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
LCVSSILSSFYYATLEESSLGLRDESMNPENPNVNLLMRLT

[illegible]

FIGURE 25

	Motif 0
human	AKFLHWLMSVYVVELLRSPFFYVTETTPQKNR
tez1	ISEIEWLVLGKRSNAXMCLSDFEKRQIFAEFIYWLNSPIIPILQSFFYITESDLNR
EST2	LKDFRWLFISD--IWFTKHNFNENLNQLAICFISWLPRLPKIIQTFFYCTEISSTVT-
p123	TREISWMQVET-SAKHPYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
	. * * * *
	Motif 1
human	LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL
tez1	TVYFRKDIWXLRCRPI-TSMKMEAFKINENNVRMDTQK-TTLPPAVIRLLPKK--NTP
EST2	IVYFRHDTWNKLITPFI VEYFKTYLVENNVCRNHNSTLS--NPNHSMRIIPKKSNEF
p123	TYYYRKNIWDVIMKMSI-ADLKKETLAEVQKEVEEWKKS-LGFAPGKLRLIPKK--TTF
	. * * * *
	Motif 2
human	RPIVNMDYVVGARTFRREKRAERLTSRVKALF-SVLNYERA
tez1	RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFKLEVYMKLLTF
EST2	RIIAIPCRGADEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
p123	RPIMTFNKKIVNSDRKTTKLTNTKLLNSHMLKTLKN-RMFKDPPGFAVFNYDDVMKKY
	* * *
	Motif 3 (A)
tez1	KKDLLKHRMFG-RKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEPVIRKYATIHATS
EST2	XQRLKKKFNNVLPelyfMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN
p123	EEFVCKWKQVGQPKLPFATHDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN
	. * * * *

FIGURE 26

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
 GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
 TCTAACTACGTGTTTCGCACTACCAAATTCAGAAAAATAGCATTACCATGCCTTCCTGG
 TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
 ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
 TCTTTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGAAAAAT
 GTTCCACAGTTTGGTCGGTACATACGCATTTCGTTGATTTATTGATCAATTATACAGTAAT
 TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAAACAGATGTAACGAACCTCATCT
 GCCGCCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
 ACTTACAGAACCAGTGACAAATAAACAATTCTTACACAAGCTCAATATAAATTCCTCTTC
 TTTTTTTCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
 GAGAGAAGCTATTTTTCCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
 TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
 GAATAGTATTTGCCCACCATTTGGAAGGGACCGTATTGGACTTGTGCGATTTGAGTAGGCA
 ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA
 AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTTATCAAGAATCTAAATCTTTTATT
 AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTGAAAAAGTTAAGATTAAA
 GGATTTTCGGTGGTTGTTTCATTTCTGATATTTGGTTTACCAAGCACAAATTTGAAAACCTT
 GAATCAATTGGCGATTTGTTTCATTTCTGGCTATTTAGACAACTAATTCCTAAAATTAT
 ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA
 TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT
 CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
 AATGAGGATTATACCAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG
 AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
 CACTCAAAAAATTTTAGAATACTTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA
 TTCTCCAACGCAAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT
 TAATAATGTCTTACCAGAGCTTTATTTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
 CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT
 TTTTCGTTAGATCTCAATATTTCTTCAATAACCAATACAGGTGTATTGAAGTTATTTAATGT
 TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
 TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT
 GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC
 TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC
 CAGTCCTAGCCAGGACACATTAATTTTAAAACCTGGCTGACGATTTCTTTATAATATCAAC
 AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
 TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
 TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAACATTCAAG
 CACAATGAATAATTTCCATATCCGTTTGAATCTAGTAAAGGGATATTTCGAAGTTTAAAT
 AGCGCTGTTTAACTAGAAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA
 CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCGGAATGTTATAAATCTGC
 TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTCAATTCGTTCTTACAACG
 CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
 TGAGGTACGATTCACCATATTGAATGGATTTTTTGGAAGCCTATCTTCAAACACATCAAA
 ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

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FIGURE 27

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREAR PALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR
AERLTSRVKALFSVLNYERA

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FIGURE 28

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAGAACAGGCTCTTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA
GAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGA
AGCCAGGCCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGC
GTGCTCAACTACGAGCGGGCGCG

CCCTGCTCAACTACGAGCGGGCGCG

FIGURE 29

MTEHHTPKSRILRFLNQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGFD
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLV
STFPNYLISILESKNWQLLLEIGSDAMHYLLSKSGIFEALPNDNYLQISGIPLFKNNVFEETVSKKRK
RTIETSITQNK SARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG
LINAQVQKQLHKVIPLVSQSTVVPKRLKLVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEILKDLETFLKLSRYESFSLHYLMSNIKISEIEWLVL
GKRSNAKMCLSDFEKRKQIFAEFIYWL YNSFIIPILQSFFYITESSDLNRNRTVYFRKDIWKLRCRPFIT
SMKMEAFEKINENNVRMDTQKTTLPPA VIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTNQT
LRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLMFR
IVKKKLLKDPEFVIRKYATIHA TSDRATKNFVSEAFSYFDMVPPFEKVVQLLSMKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPOGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVD DFLFITVNKKDAKKFLNLSLRGFEEKHNFSTSLEKTVINFENSGIINNTFFNESKKRMPFFG
FSVNMRLSDTLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCNI
YRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFCL
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVFLHRRJAD

FIGURE 30

ggtaccgatttactttctttctcacaagctaattgcttctcgaacgctcctaaatctctggaaatattttacaagaactcaataacaataccaagtcaaattccaatatgaagg
 tgtatttagtgatcgataatatttctatttaccggtcgttaccagataaggacaaaaagaacaacttcttccccctaaagacttttacttttataatttacttttcaaatatattcg
 ggttcgcttacttttaacgttggtactgttttagctgctacttctagccaaccgctgttttctaccccgctattggatatagctcttggagtagctcacagaatccttcaaatctt
 ctgatgagactatattagattacagtcggtgcatattcttaacatggagccttacacttttagatgagtcacgtcgcgatgaggatttggatcatccaacgtttgcttg
 aaaaggttgataattattgcaaatcatgtccttagtggtggaatccgcaaggtttttgatgctgacacgtctagcatgattgagatattcaaaaatttctatccactacaa
 ctctttaacgcggtttattttctattttctatttctatgttgcctcaaatatgtatcatctgtattaggctttttcgttttactcctggaatcgtaccttttctacttccccctaatg
 aataatctaaattagtttgcctataattgatagtagtagaaagattggtgattctactcgttaattgtattagtttaagatactttgcaaacatttattagctatcattatataaaa
 aaaaatcctataattataatattaatcaatatttgcggtcactatttttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaattggttacttgaacttgcAT
 GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTA
 CCTTAAATGATTATGTACAACCTTGTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAA
 CGCTTGAGAAGCGATGTACAAACGTCCTTTTCTATTTTCTTCATTGACTGTAGTCGGCTTCGACAGT
 AAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAAATGCTCACAGTCAGAGGtatatatatttttggattttttctattcg
 ggatagctaatatatggcgagCTAATAGCGAATGTTGTAAACAGATGTTTCGATGAAAGTTTTGAGCGTCGAAGGA
 ATCTACTGATGAAAGGGTTTTCCATGtaaggatttcaattgtgaaatatttactcgtcaattactgtttcaagagattgtatttaaccgataaagAA
 TCATGAAGATTTTCGAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCTAATTA
 CCTTATATCTATACTTGAGTCAAAAAATTGGCAACTTTTGTAGAAATgtaataaccggttaagattgtgcgcaacttgaaca
 agactgacaagtatagTATCGGCAGTGATGCCATGCATTACTTATTATCCAAAGGAAGTATTTTGGAGGCTCTTC
 CAAATGACAATTACCTTCAGATTTCTGGCATAACCACTTTTAAAAATAATGTGTTTGAGGAACTGTGT
 CAAAAAAGAAAGCGAACCATTGAAACATCCATTACTCAAAATAAAAGCGCCCGCAAAGAAGTTTC
 CTGGAATAGCATTTCATTAAGTAGGTTTAGCATTTTTACAGGTCATCCTATAAGAAGTTTAAGCAAGgt
 aactaactgttatcttcataactaatttagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG
 TGGCTTCAATGGATTTTTCGAAGCAATTTGGACTTATAAACGCATTTCAAGTGAAGCAATTGCACAA
 AGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCCTAAAGGTATACCCTTTAATTGA
 ACAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGA
 CCCCCAGATGATGAAAAAATCCTTAGTTATTCTTAAAGCCGAACCAGGTGTTTGCCTTCTTCGATC
 CATTCTGTTTCGAGTGTTTCTAAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAGg
 tattgtataaaattattaccactaacgattttaccagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTAC
 ATTATTTAATGAGTAACATAAAGGtaaatatgccaaatttttaccattaattaacaatcagATTTGAGAAATTGAATGGCTAGT
 CCTTGGAAGAAAGGTCAAATGCGAAAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAATATTTGCGG
 AATTCATCTACTGGCTATACAATTCGTTTATAATACCTATTTTACAATCTTTTTTTTATATCACTGAATC
 AAGTGATTTACGAAATCGAACTGTTTATTTTGAAGAAAGATATTTGAAACTCTTGTCGCGACCTTTAT
 TACATCAATGAAAATGGAAGCGTTTGAAGAAATAAACGAGgtattttaagatttttgcataaagtaattttcagAACAA
 TGTTAGGATGGATACTCAGAAAACACTTTGCCTCCAGCAGTTATTCGTCTATTACCTAAGAAGAATAC
 CTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAAGtattaatttttggatcaatgtactttacttctaatctatttagg
 cagATGGGTTCAAACAAAAAATGTTAGTCAGTACGAACCAAACTTTACGACCTGTGGCATCGATACTG
 AAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGGAGGTTTACATGAAGCTTCTTACT
 TTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGgttaattataatgcgcatcctcattattaattttcagGCGTAAGAAG
 TATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTGATGTTTCGGATTGTT
 AAAAAAGAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCG
 AGCTACAAAAAATTTGTTAGTGAGGCGTTTTCTATTgtaagtttatttttattggaatttttaacaaattcttttagTTGATAT
 GGTGCTTTTGAAGAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTGATTGTTGT
 GGATTATTGGACCAAAAGTTCTTCTGAAATTTTTAAATGCTCAAGGAACATCTCTCTGGACACATTGT
 TAAAGgtataccaattgtgaattgaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTC
 AGGGCTCAATTCTGTCTATCTTTTGTGTCAATTTCTATATGGAAGATTGATTGATGAATACCTATCGTT
 TACGAAAAAGAAAGGATCAGTGTTGTTACGAGTAGTCGACGATTTCTCTTTATAACAGTTAATAAAA
 AGGATGCAAAAAAATTTTGAATTTATCTTTAAGAGgtgagtgctgtcattcctaagttctaaccgttgaagGATTTGAGAA
 ACACAATTTTCTACGAGCCTGGAGAAAACAGTAATAAATTTGAAAAATAGTAATGGGATAATAACA
 ATACTTTTTTAAATGAAAGCAAGAAAGAAATGCCATTCTTCGGTTTCTCTGTGAACATGAGGTCTCTTG
 ATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAGAGCTGACGAAAC
 ATATGGGGAAATCTTTTTTTTACAAAATCTAAAGgtatactgtgaactgaataatagctgacaataatcagATCGAGCCTTGC
 ATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTCATTCTTGCTGCAATATATATAG
 GCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATCCCC
 AAAGAATGTTTATAACGGgtgagtgacttattttaactgaagaagtcatttaaaccttagATCTTTTGAATGTTATTGGAAGAAAA
 ATTTGGAAGAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGCTCTCTGCAGAAGTCAA

FIGURE 30 (cont.)

ATGgtacgtgtcgggtctcgagacttcagcaatattgacacatcagGCTTTTTTGTCTTGAATGAGAGATGGTTTGAAACCCCTCTT
TCAAATATCATCCATGCTTCGAACAGCTAATATACCAATTTTCAGTCATTGACTGATCTTATCAAGCCGC
TAAGACCAGTTTTGCGACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAAtgicattttcaattattatatacatcctt
tattactgggtgtcttaacaatattattactaagtatagctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagtttgattgactgtctt
atccttatacttttaagaagattgacagtgggtgctgactactgccacatgccattaacgggagtggttaacattaaaagtaatacatgaggctaattctccttcatttag
aataaggaaagtgttttctataatgaataatgccgcactaatgcaaaaagacgaagattatcttctaaacaagggggattaagcatatccgaaggaaaagagagtaatat
accagtggtgtgaagaaagcaaggataatttgaacaagcttctgcagatgacaggctaaatttggtagccgaatttggtaaaagcccaggttatccatggtggccg
gccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcatttaattgtcttatataaggtttgttttctgacttcaatttgcattgggtgaaaagaaata
gtgtaagccattattggattccgaaatagccaaatttcttggttctcaaaagcgaagtctaaagaacttattgaagcttatgaggcttcaaaaactcctcctgatttaaggag
gaatctccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttgcaaaaagaaaatatcatgggagacatcttgaatcagatgcgga
gagtatctccagcggatccttgatgtcaataacttctatttctgaaatgtatggtcctactgtcgttcgacttctcgtagctctacgcagttaagtaccaaaggtacc

FIGURE 31

EST2 pep	FFYCTEISST VTIVYFRHDT WN----KLIT P-----FIVE YFK-TYLVEN	40
Euplotes pep	FFYVTEQOKS YSKTYYYRKN IWDVI-MKMS IAD---LKK ETLA--EVQE	43
Trans of tetrahymen	-----KHKE GSQIFYRKP IWKLVSCLTI VKVRIQFSEK NKQMKNFYQ	44
Consensus	FFY.TE..K. .S..YYRK. IW...-KL.. ----F..KV..	50
EST2 pep	NVCRNHNSY- ----- TLSNFNHSTV-RLTPKKSNE FRITAIPCRG	79
Euplotes pep	KEVEEWKKS- ----- --GFAPGCK-RLTPKKT-- FRHMTFNKK	78
Trans of tetrahymen	KIQLEENLE KVEEKLPED SFQKYPQCK-RLTPKKS-- FRHMTFLRK	92
Consensus	K...E..... -----F..CKE-RLTPK...-- FRHMTF.RK	100
EST2 pep	ADEESFTIYK ENHKNAIQPT OKILEYRNK RPTSFTKIYS FTQIADRIKE	129
Euplotes pep	IVNSDRKTTK LTTNTKLLNS HLMLKTEKN- -----RMFK -DPFGFAVFN	120
Trans of tetrahymen	DKQKNIK--- LNLNQILMDS QLVFRNKKD- -----ML-G -QKIGYSVFD	130
ConsensusK..K LN.N..L..S QL.L. LKN- -----.... -..IG..VF.	150
EST2 pep	FKQRLKKEN NVL----- -PFLYFMKFD VKSCYD	157
Euplotes pep	YD-DVMKKYE EFVCKWKQVG QPKLFFAIMD IEKCYD	155
Trans of tetrahymen	NK-QISEKFA QFIEKWQKNG RPKLYYVTL- -----	158
Consensus	.K-...KKF. .F..KWK..G .S.LYF.T.D ...CYD	186

FIGURE 32

S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

SECRET

FIGURE 33

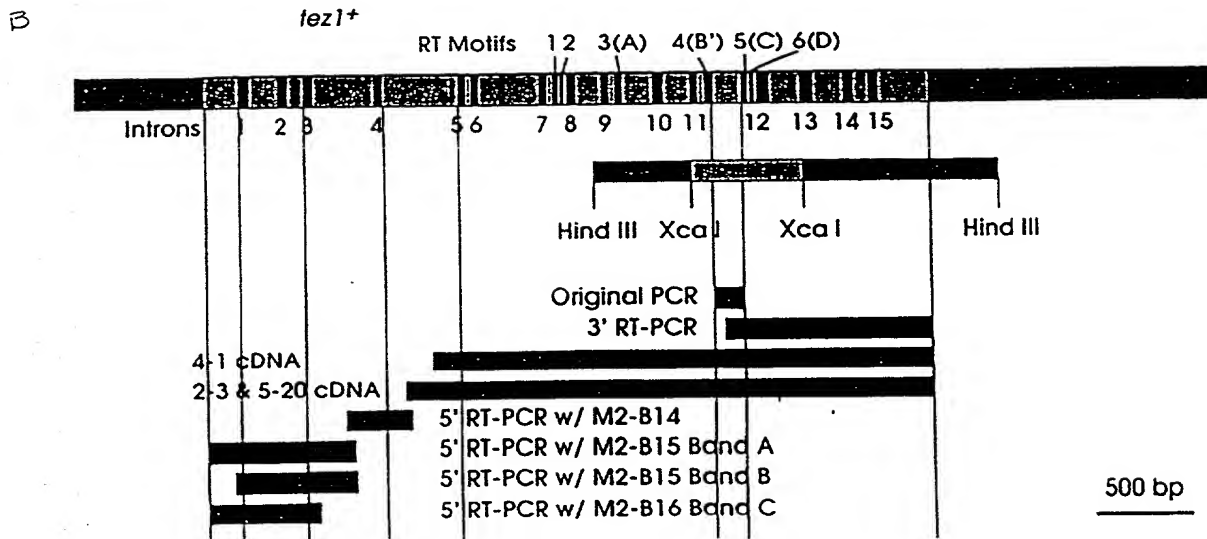
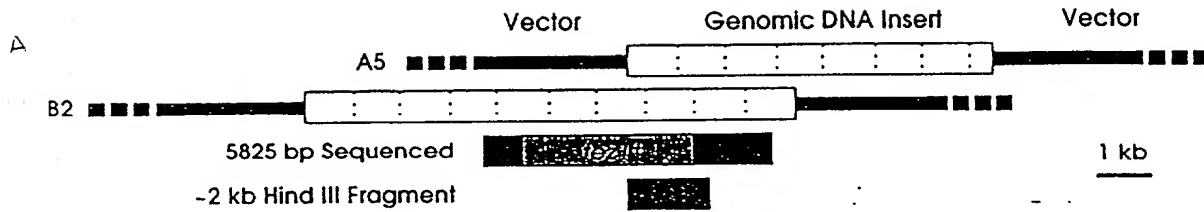


FIGURE 34

Poly 4

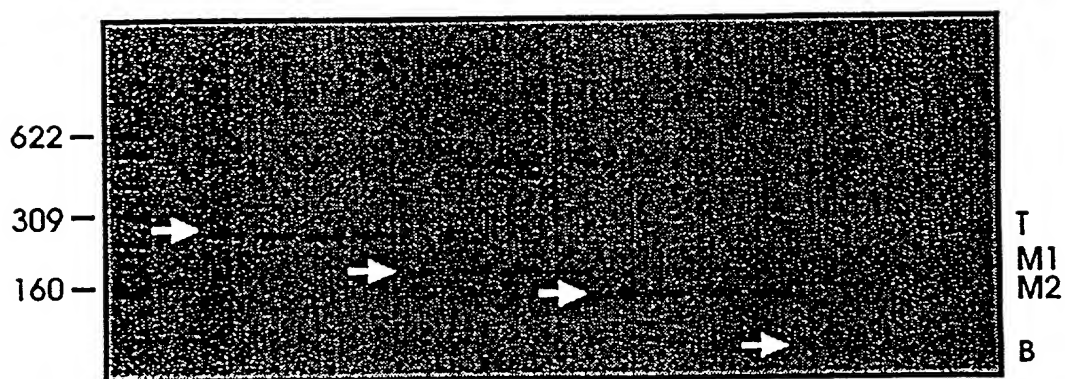
	t		t		c			
	t	a	a	g	c	c	t	c g
5'-	cag	acc	aaa	gga	att	cca	taa	gg -3'
	Q	T	K	G	I	P	Q	G

4 (B')

5 (c')

	D	D	Y	L	L	I	T	
3'-	ctg	ctg	atg	gag	gag	tag	tgg	-5'
	a	a	a	a	a	a	a	
			t	t	t	t		
					c	c		
					<u>Poly 1</u>			

FIGURE 35



Motif B' (4)
QTKGIPQG

Motif C (5)
DDYLLIT

FIGURE 36

PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

Ot	LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123	KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2	SILSSF LCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sc_p103	DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS
	. * . * . *

Q K V G I P Q G
 caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

Poly 4
 t t c
 t a a g c c t c g
 cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
 tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

K G I P S G S I L S S F L C H F Y M

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
 CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc
 CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

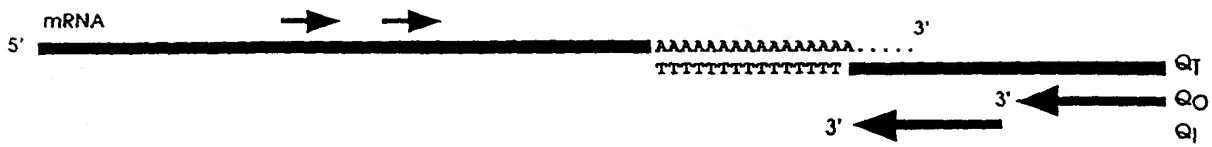
<---- ctg ctg atg gag gag tag tgg
 a a a a a a a a
 t t t t
 c c

Poly 1

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence.
 D D F L F I T

FIGURE 37

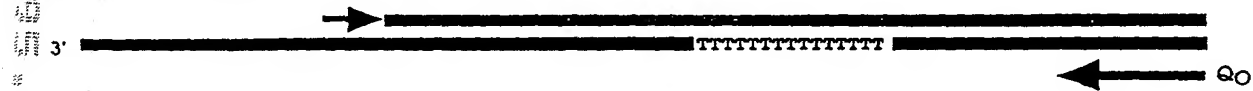
3' RT PCR Strategy



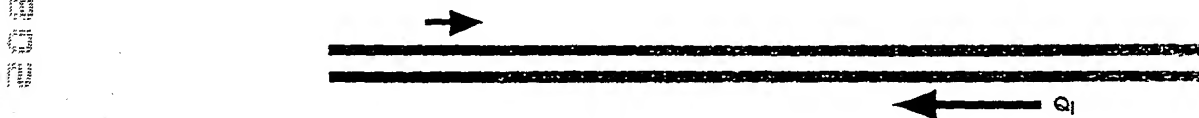
1. Synthesis of cDNA with Q_T Primer.



2. First Round PCR Using Outside Primer and Q_O Primer.



3. Second Round PCR Using Inside Primer and Q_I Primer.



4. Sequence Second Round PCR Products Using Inside Primer or Q_I Primer.



FIGURE 38

A

-Size Selected Libraries from P. Nurese

- 3 ~ 4 kb
- 5 ~ 6 kb
- 7 ~ 8 kb
- 11 ~ 12 kb

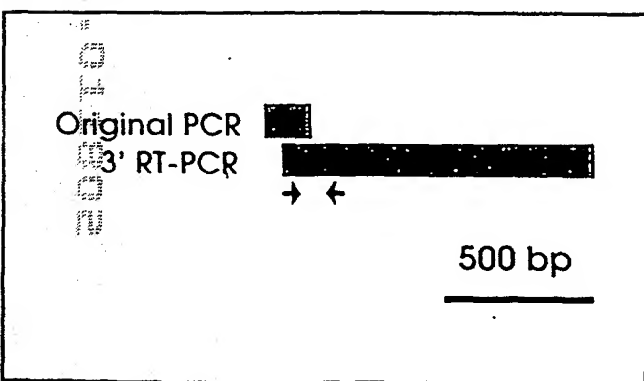
-Libraries from J.A. Wise

- Sau 3a Partial Digest
- Hind III Partial Digest

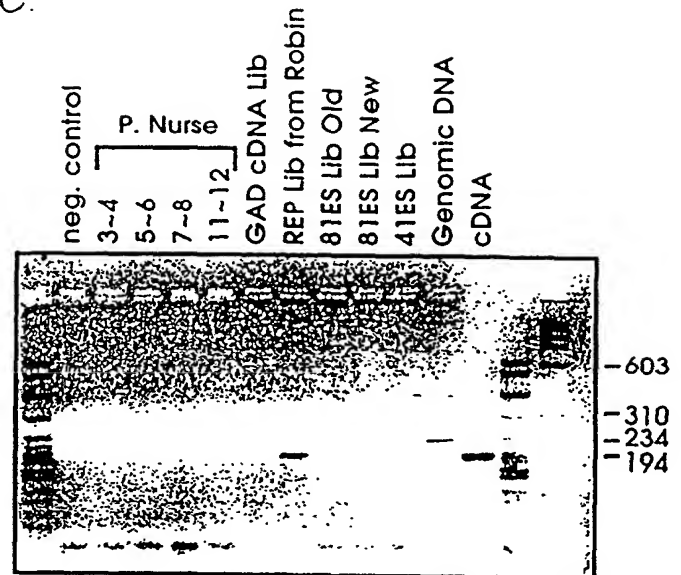
cDNA Libraries

- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

B.



C.



D.

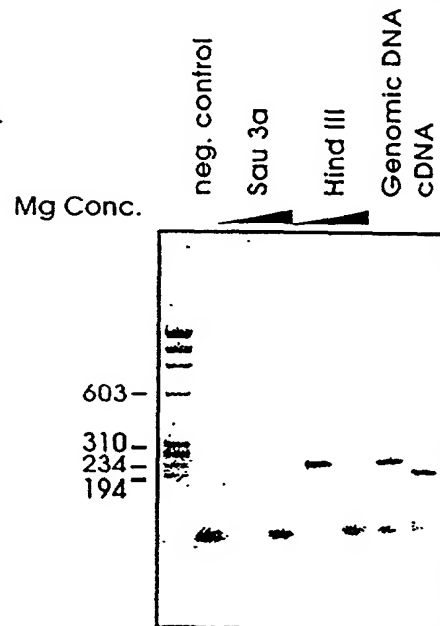


FIGURE 39

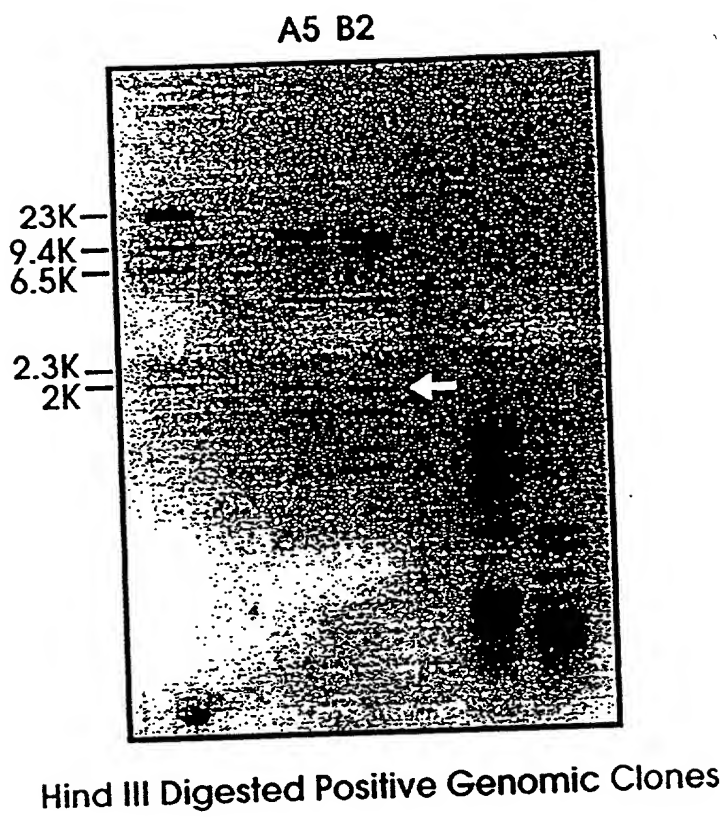
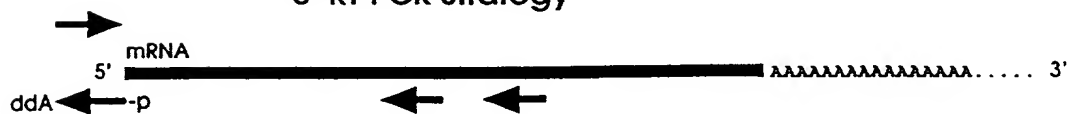


FIGURE 40

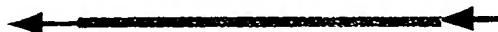
5' RT PCR Strategy



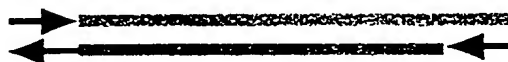
1. Synthesis of cDNA with Specific Downstream Primer.



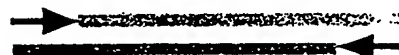
2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.



3. First Round PCR



4. Second Round PCR



Motif 0

Motif 1	Motif 2	K
h h n K	h R h	R

```

AVIRLLPKK--NTFRLITN-LRKRF ... (61) ...
SKMRIIPKKSNNEFRIIAIPCRGAD ... (62) ...
GKLR_LIPKK--TTFRPIMTFNKKIV ... (61) ...
  *   *   *   *   *

```

Motif	3 (A)	AF
h	hDh	GY

S.p. Tez1p ZKYFVRIDIKSCYDRIKQDLMFRIVK ... (89) ...
S.c. Est2p ELYFMKFDVKSCYDSIPRMECMRILK ... (75) ...
E.a. p123 KLFFATMDIEKCYDSVNREKLSTFLK ... (107) ...
 * * *** *

Motif 4 (B')

		hPQG	pP	hh	h	
S.p.	Tez1p	YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF				... (6) ...
S.c.	Est2p	YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF				... (8) ...
E.a.	p123	YKQTKGIPQGLCVSSILSSFYYATLEESSLGF				... (14) ...
		* * *				

Y Motif 5(C)

	h	F	DDhhh	Gh	h	CK	h	
S.p. Tez1p	VLLRVVDDFLFITVNKKDAKKFLNL	SLRGFEKHNFST	SLEKTVINFENS					(205)
S.c. Est2p	LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS							(173)
E.a. p123	LLMRLTDDYLLITTTQENNAVL	FTIEKLINVSRENGFKFNMKKLQTSFPLS						(209)
	**	*	*			*	*	

Motif 6 (D)

Gh h cK h

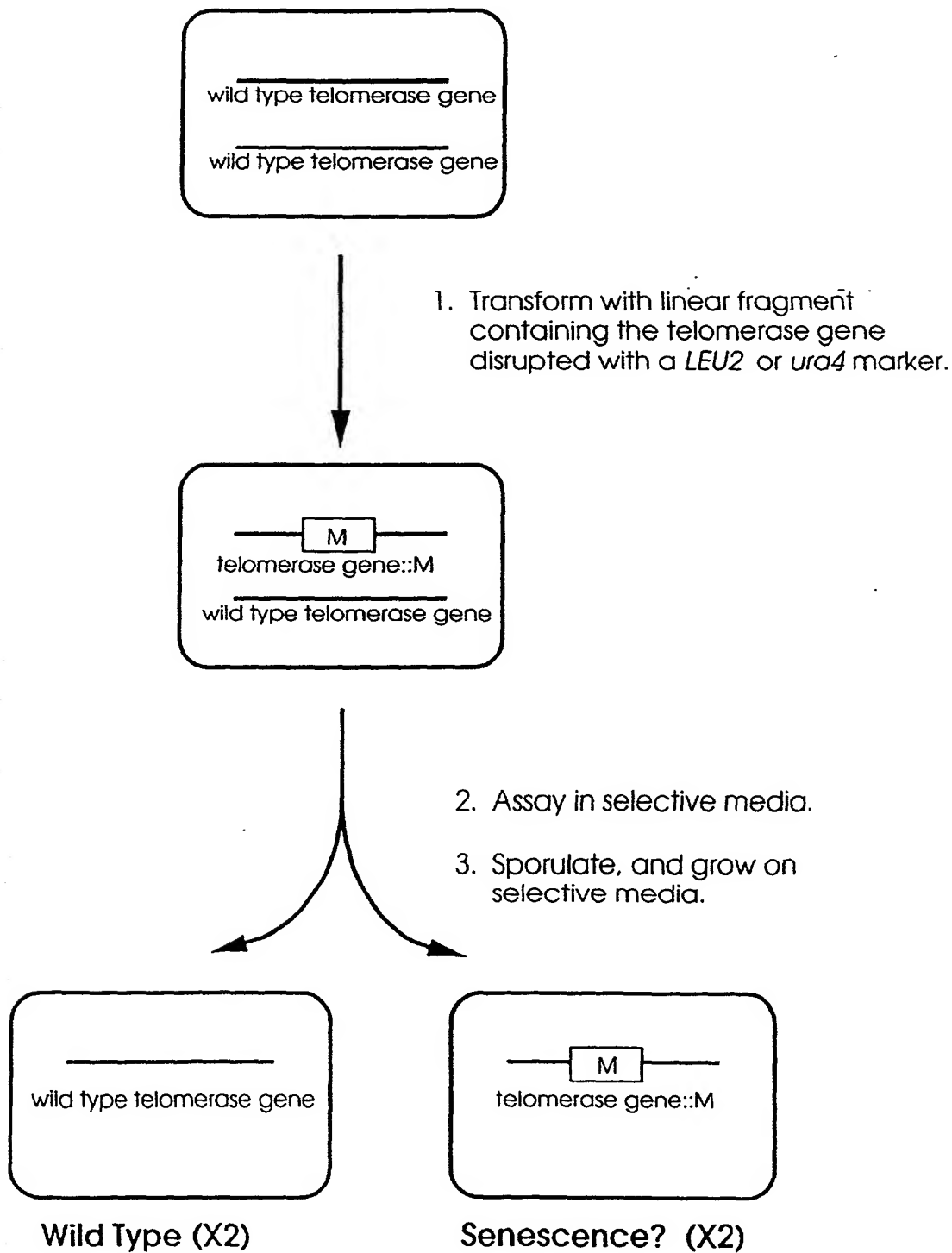
[illegible]

6

[illegible]

FIGURE 43

Disruption strategy for the putative telomerase genes.



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

[illegible]

An Example of Confirmation of *tez1* disruption By PCR

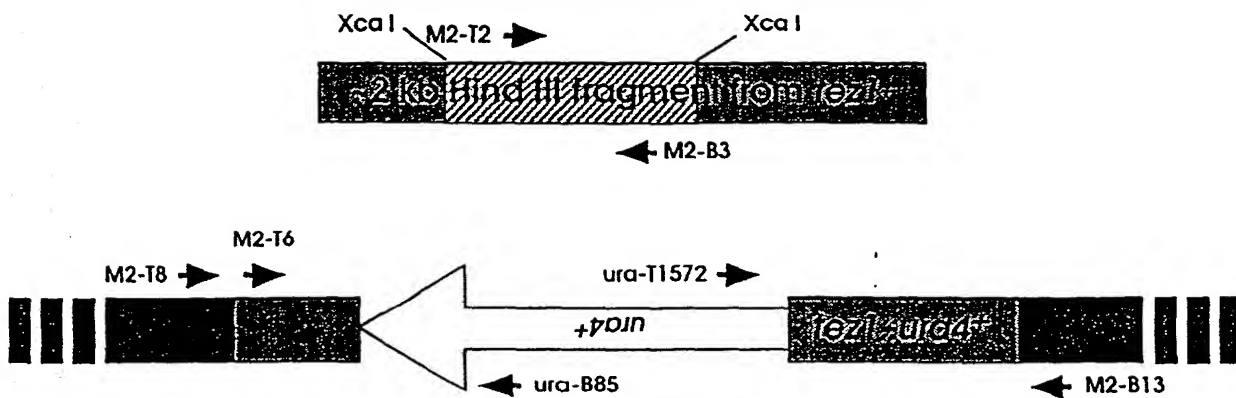
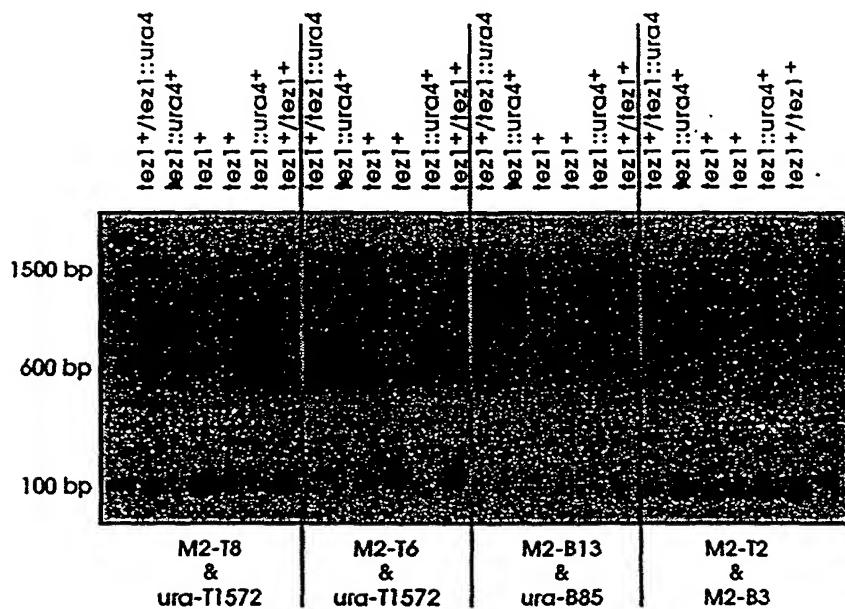


FIGURE 45

Tez1 disruption causes progressive shortening of telomeres in *S. pombe*

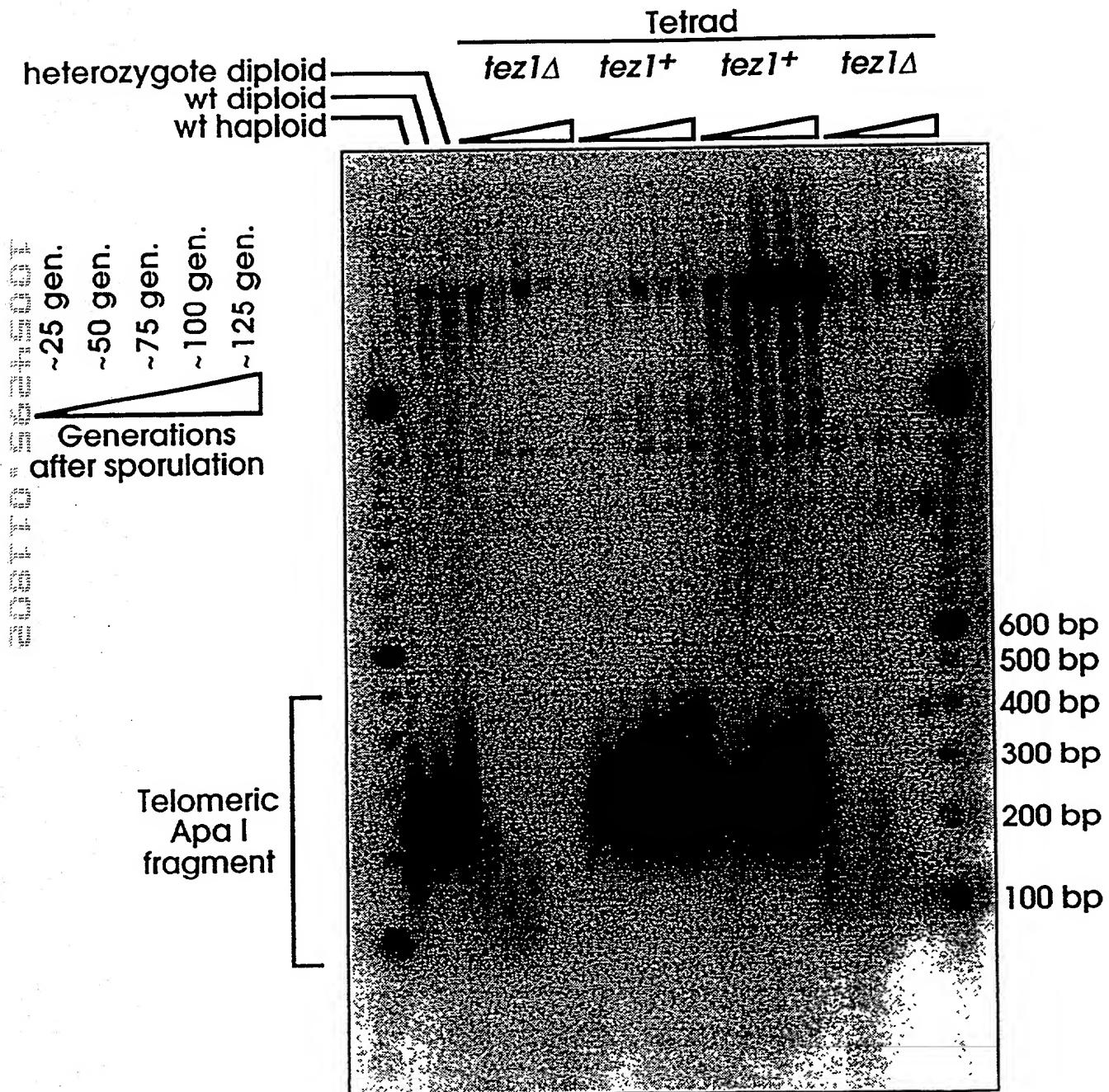


FIGURE 46

1 ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga 80
 81 actcaataacaataccaagtcaaattccaatatgaagggtgttatttagtgatcgataatatttctattttatcgggtcggtta 160
 161 ccaagtataaggacaaaaagaacaacttccttccccctaaagacttttactttattaatttacttttcaaatatatttcg 240
 241 ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgctcattggatat 320
 321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtcctgcatattc 400
 401 ttaacatggagccttacacttttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag 480
 481 gttgataattatttgcaaaatcatgtccttagtggtggtgaatccgcgaaagttttttgatgcttgacacgtctagcatg 560
 561 attgagatattcaaaaatttctatccactacaactcctttaacgcgggttttatttttctattttctattctcatgttggt 640
 641 ccaaatatgtatcatctcgtatttaggctttttccggttttactcctggaatcgtaaccttttctactattccccctaatga 720
 721 ataatctaaattagtttcgcttataattgatagtagtagaaagattgggtgattctactcgtgtaatgttattagtttaaa 800
 801 gatacttttgcaaaacattttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880
 881 actattttatttaaaacggttatgatcagtaggacactttgcatatatatagtttatgcttaatgggttacttgtaacttgc 958

 959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
 1 M T E H H T P K S R I L R F L E N Q Y V 20
 1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
 21 Y L C T L N D Y V Q L V L R G S P A S S 40
 1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138
 41 Y S N I C E R L R S D V Q T S F S I F L 60
 1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
 61 H S T V V G F D S K P D E G V Q F S S P 80

FIGURE 46 (cont.)

1199	AAA TGC TCA CAG TCA GAG	gtatatatatatgttttgatttttttctattcgggatagctaatatatgggcag	1272
81	K C S Q S E		86
1273	CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA	1332	
87	L I A N V V K Q M F D E S F E R R R N L	106	
1333	CTG ATG AAA GGG TTT TCC ATG	gtaagggtatttctaattgtgaaatattttacctgcaattactgtttcaaagaga	1405
107	L M K G F S M	113	
1406	ttgtattttaaccgataaag	AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT	1469
114		N H E D F R A M H V N G V Q N	128
1470	GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA	1529	
129	D L V S T F P N Y L I S I L E S K N W Q	148	
1530	CTT TTG TTA GAA AT	gtaaataccggttaagatgttgcgcaactttgaacaagactgacaagtatag T ATC GGC	1601
149	L L L E I	I G	155
1602	AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC	1661	
156	S D A M H Y L L S K G S I F E A L P N D	175	
1662	AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG	1721	
176	N Y L Q I S G I P L F K N N V F E E T V	195	
1722	TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA	1781	
196	S K K R K R T I E T S I T Q N K S A R K	215	
1782	GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT	1841	
216	E V S W N S I S I S R F S I F Y R S S Y	235	
1842	AAG AAG TTT AAG CAA G	gtaactaataactgttatccttcataactaatttttag AT CTA TAT TTT AAC	
1907			
236	K K F K Q D	L Y F N	245
1908	TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG	1967	
246	L H S I C D R N T V H M W L Q W I F P R	265	
1968	CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA	2027	
266	Q F G L I N A F Q V K Q L H K V I P L V	285	
2028	TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA	2087	
286	S Q S T V V P K R L L K V Y P L I E Q T	305	
2088	GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT	2147	
306	A K R L H R I S L S K V Y N H Y C P Y I	325	
2148	GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG	2207	
326	D T H D D E K I L S Y S L K P N Q V F A	345	
2208	TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA	2267	
346	F L R S I L V R V F P K L I W G N Q R I	365	
2268	TTT GAG ATA ATA TTA AAA G	gtattgtataaaattttattaccactaacgattttaccag AC CTC GAA ACT	2336
366	F E I I L K D	L E T	375

FIGURE 46 (cont.)

2337	TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG	2396	
376	F L K L S R Y E S F S L H Y L M S N I K	395	
2397	gtaatatgccaaatttttttaccattaattaacaatcag	ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA	2465
396		I S E I E W L V L G	405
2466	AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG	2525	
406	K R S N A K M C L S D F E K R K Q I F A	425	
2526	GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT	2585	
426	E F I Y W L Y N S F I I P I L Q S F F Y	445	
2586	ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA	2645	
446	I T E S S D L R N R T V Y F R K D I W K	465	
2646	CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA-ATA AAC GAG	2705	
466	L L C R P F I T S M K M E A F E K I N E	485	
2706	gtatttttaaagtattttttgcaaaaagctaataatttttcag	AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT	2775
486		N N V R M D T Q K T	495
2776	ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG	2835	
496	T L P P A V I R L L P K K N T F R L I T	515	
2836	AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaatttttggtcatcaatgtactttacttctaattctatta	2906	
516	N L R K R F L I K	524	
2907	ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG	2967	
525	M G S N K K M L V S T N Q T L R P V	542	
2968	GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG	3027	
543	A S I L K H L I N E E S S G I P F N L E	562	
3028	GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat	3088	
563	V Y M K L L T F K K D L L K H R M F G	581	
3089	tatataatgcgcgattcctcattattaattttgcag	G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA	3155
582		R K K Y F V R I D I	591
3156	AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC	3215	
592	K S C Y D R I K Q D L M F R I V K K K L	611	
3216	AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT	3275	
612	K D P E F V I R K Y A T I H A T S D R A	631	
3276	ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttttcattggaattttttaacaa	3343	
632	T K N F V S E A F S Y F	643	
3344	attcttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA	3405	
644		D M V P F E K V V Q L L S M K T	659
3406	TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT	3465	
660	S D T L F V D F V D Y W T K S S S E I F	679	
3466	AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattggtgaattgtaataaca	3532	
680	K M L K E H L S G H I V K	692	

100

3533	cta	aatga	actag	ATA	GGA	AAT	TCT	CAA	TAC	CTT	CAA	AAA	GTT	GGT	ATC	CCT	CAG	GGC	TCA	3593	
693				I	G	N	S	Q	Y	L	Q	K	V	G	I	P	Q	G	S	708	
3594	ATT	CTG	TCA	TCT	TTT	TTG	TGT	CAT	TTC	TAT	ATG	GAA	GAT	TTG	ATT	GAT	GAA	TAC	CTA	TCG	3653
709	I	L	S	S	F	L	C	H	F	Y	M	E	D	L	I	D	E	Y	L	S	728
3654	TTT	ACG	AAA	AAG	AAA	GGA	TCA	GTG	TTG	TTA	CGA	GTA	GTC	GAC	GAT	TTC	CTC	TTT	ATA	ACA	3713
729	F	T	K	K	K	G	S	V	L	L	R	V	V	D	D	F	L	F	I	T	748
3714	GTT	AAT	AAA	AAG	GAT	GCA	AAA	AAA	TTT	TTG	AAT	TTA	TCT	TTA	AGA	G	gtgagttgctgtcattcc				3777
749	V	N	K	K	D	A	K	K	F	L	N	L	S	L	R	G					764
3778	taagttcta	aaccgttgaag	GA	TTT	GAG	AAA	CAC	AAT	TTT	TCT	ACG	AGC	CTG	GAG	AAA	ACA	GTA				3840
765				F	E	K	H	N	F	S	T	S	L	E	K	T	V				778
3841	ATA	AAC	TTT	GAA	AAT	AGT	AAT	GGG	ATA	ATA	AAC	AAT	ACT	TTT	TTT	AAT	GAA	AGC	AAG	AAA	3900
779	I	N	F	E	N	S	N	G	I	I	N	N	T	F	F	N	E	S	K	K	798
3901	AGA	ATG	CCA	TTC	TTC	GGT	TTC	TCT	GTG	AAC	ATG	AGG	TCT	CTT	GAT	ACA	TTG	TTA	GCA	TGT	3960
799	R	M	P	F	F	G	F	S	V	N	M	R	S	L	D	T	L	L	A	C	818
3961	CCT	AAA	ATT	GAT	GAA	GCC	TTA	TTT	AAC	TCT	ACA	TCT	GTA	GAG	CTG	ACG	AAA	CAT	ATG	GGG	4020
819	P	K	I	D	E	A	L	F	N	S	T	S	V	E	L	T	K	H	M	G	838
4021	AAA	TCT	TTT	TTT	TAC	AAA	ATT	CTA	AG	gtatactgtgtaactgaataatagctgacaaataatcag	A	TCG								4089	
839	K	S	F	F	Y	K	I	L	R											S	848
4090	AGC	CTT	GCA	TCC	TTT	GCA	CAA	GTA	TTT	ATT	GAC	ATT	ACC	CAC	AAT	TCA	AAA	TTC	AAT	TCT	4149
849	S	L	A	S	F	A	Q	V	F	I	D	I	T	H	N	S	K	F	N	S	868
4150	TGC	TGC	AAT	ATA	TAT	AGG	CTA	GGA	TAC	TCT	ATG	TGT	ATG	AGA	GCA	CAA	GCA	TAC	TTA	AAA	4209
869	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R	A	Q	A	Y	L	K	888
4210	AGG	ATG	AAG	GAT	ATA	TTT	ATT	CCC	CAA	AGA	ATG	TTC	ATA	ACG	G	gtgagtacttatttttaactaga				4274	
889	R	M	K	D	I	F	I	P	Q	R	M	F	I	T	D						903
4275	aaagtcatta	attaac	cttag	AT	CTT	TTG	AAT	GTT	ATT	GGA	AGA	AAA	ATT	TGG	AAA	AAG	TTG	GCC		4339	
904					L	L	N	V	I	G	R	K	I	W	K	K	L	A		917	
4340	GAA	ATA	TTA	GGA	TAT	ACG	AGT	AGG	CGT	TTC	TTG	TCC	TCT	GCA	GAA	GTC	AAA	TG	gtacgtgtc	4401	
918	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W		935	
4402	ggtctcgagacttcag	caatattgacacatcag	G	CTT	TTT	TGT	CTT	GGA	ATG	AGA	GAT	GGT	TTG	AAA						4468	
936				L	F	C	L	G	M	R	D	G	L	K						946	
4469	CCC	TCT	TTC	AAA	TAT	CAT	CCA	TGC	TTC	GAA	CAG										

FIGURE 46 (cont.)

4666 gctgacccccaaagcaagcatactataggattttctagtaaagtaaaattaatctcgttattagttttgattgacttgct 4745
4746 ttatccttatacttttaagaaagattgacagtggttgctgactactgccacatgccattaaacgggagtggttaaaca 4825
4826 ttaaaagtaatacatgaggctaattctcctttcatttagaataaggaaagtggttttctataatgaataatgccgcacta 4905
4906 atgcaaaaagacgaagattatcttctaacaagggggattaagcatatccgaaggaaaagagagtaatataccagtggt 4985
4986 gttgaagaaagcaaggataatttgaacaagcttctgcagatgacaggctaatttttggtgaccgaattttggtaaaagc 5065
5066 cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaataactaatagctcattta 5145
5146 atgtcttatataagggttttgttttttctgacttcaattttgcatgggtgaaaagaaatagtggttaagccattattggat 5225
5226 tccgaaatagccaaatttcttggttcctcaaagcggaagtctaagaacttattgaagcttatgaggcttcaaaaaactcc 5305
5306 tcctgatttaaaggaggaatctccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaattttttgc 5385
5386 aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggaatccttgatgtcaata 5465
5466 acttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtagc 5544

4666
4746
4826
4906
4986
5066
5146
5226
5306
5386
5466

FIGURE 47

1
 met ser val tyr val val glu leu leu
 ATG AGT GTG TAC GTC GTC GAG CTG CTC
 GCCAAGTTCCTGCACTGGCTG
 10 20
 arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
 AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG
 30
 leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
 CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT
 40 50
 gly ile arg gln his leu lys arg val gln leu arg glu leu ser
 GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG
 60
 glu ala glu val arg gln his arg glu ala arg pro ala leu leu
 GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG
 70 80
 thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
 ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG
 90
 ile val asn met asp tyr val val gly ala arg thr phe arg arg
 ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA
 100 110
 glu lys ala glu arg leu thr ser arg val lys ala leu phe
 GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC
 120
 ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
 AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC
 130 140
 ala ser val leu gly leu asp asp ile his arg ala trp arg thr
 GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC
 150
 phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
 TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC
 160 170
 phe val lys val asp val thr gly ala tyr asp thr ile pro gln
 TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG
 180
 asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
 GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

FIGURE 47 (cont.)

190	thr	tyr	cys	val	arg	arg	tyr	ala	val	val	200	gln	lys	ala	ala	met										
	ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC		CAG	AAG	GCC	GCC	ATG										
											210	gly	thr	ser	ala	arg	pro	ser	arg	ala	thr	ser	tyr	val	gln	cys
												GGC	ACG	TCC	GCA	AGG	CCT	TCA	AGA	GCC	ACG	TCC	TAC	GTC	CAG	TGC
220	gln	gly	ile	pro	gln	gly	ser	ile	leu	ser	230	thr	leu	leu	cys	ser										
	CAG	GGG	ATC	CCG	CAG	GGC	TCC	ATC	CTC	TCC		ACG	CTG	CTC	TGC	AGC										
											240	leu	cys	tyr	gly	asp	met	glu	asn	lys	leu	phe	ala	gly	ile	arg
												CTG	TGC	TAC	GGC	GAC	ATG	GAG	AAC	AAG	CTG	TTT	GCG	GGG	ATT	CGG
250	arg	asp	gly	leu	leu	leu	arg	leu	val	asp	260	asp	phe	leu	leu	val										
	CGG	GAC	GGG	CTG	CTC	CTG	CGT	TTG	GTG	GAT		GAT	TTC	TTG	TTG	GTG										
											270	thr	pro	his	leu	thr	his	ala	lys	thr	phe	leu	arg	thr	leu	val
												ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	ACC	TTC	CTC	AGG	ACC	CTG	GTC
280	arg	gly	val	pro	glu	tyr	gly	cys	val	val	290	asn	leu	arg	lys	thr										
	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	GTG		AAC	TTG	CGG	AAG	ACA										
											300	val	val	asn	phe	pro	val	glu	asp	glu	ala	leu	gly	gly	thr	ala
												GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC	CTG	GGT	GGC	ACG	GCT
310	phe	val	gln	met	pro	ala	his	gly	leu	phe	320	pro	trp	cys	gly	leu										
	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC		CCC	TGG	TGC	GGC	CTG										
											330	leu	leu	asp	thr	arg	thr	leu	glu	val	gln	ser	asp	tyr	ser	ser
												CTG	CTG	GAT	ACC	CGG	ACC	CTG	GAG	GTG	CAG	AGC	GAC	TAC	TCC	AGC
340	tyr	ala	arg	thr	ser	ile	arg	ala	ser	leu	350	thr	phe	asn	arg	gly										
	TAT	GCC	CGG	ACC	TCC	ATC	AGA	GCC	AGT	CTC		ACC	TTC	AAC	CGC	GGC										
											360	phe	lys	ala	gly	arg	asn	met	arg	arg	lys	leu	phe	gly	val	leu
												TTC	AAG	GCT	GGG	AGG	AAC	ATG	CGT	CGC	AAA	CTC	TTT	GGG	GTC	TTG
370	arg	leu	lys	cys	his	ser	leu	phe	leu	asp	380	leu	gln	val	asn	ser										
	CGG	CTG	AAG	TGT	CAC	AGC	CTG	TTT	CTG	GAT		TTG	CAG	GTG	AAC	AGC										

FIGURE 47 (cont.)

390

leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400

ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

410

420

gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430

arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

440

450

val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460

arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

470

480

thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490

pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

500

510

pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520

his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

530

540

thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550

arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

560

564

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TGA GTGAGTGTGTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCGGGCTGAGGC

CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

FIGURE 47 (cont.)

AGGCTGGCGTTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT
CCCCACATAGGAATAGTCCATCCCCAGATTGCGCATTGTTTACCCTTCGCCCTGCCTTCC
TTTGCCTTCCACCCCCACCATTTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT
TTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 48

Motif -1
 Ep p123 ...LVVSLIRCFYVTEQQKSYSKT...
 Sp Tez1 ...FIIPILQSFFYITESSDLRNRT...
 Sc Est2 ...LIPKIIQTFFYCTEISSTVTIV...
 Hs TCP1 ...YVVELLRSFFYVTETTFQKNRL...
 consensus FFY TE

Motif 0
 Ep p123 ...KSLGFAPGKLRRLIPKKT--TFRPIMTFNKKIV...
 Sp Tez1 ...QKTTLPPAVIRLLPKKN--TFLITNLRKRFL...
 Sc Est2 ...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...
 Hs TCP1 ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
 consensus R PK R I

Motif A
 Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...
 Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
 Sc Est2 ...PELYFMKFDVKSCYDSIPRMECMRILK...
 Hs TCP1 ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
 consensus F D YD

Motif B
 Ep p123 ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
 Sp Tez1 ...GNSQYLOKVGIPQGSILSSFLCHFYME...
 Sc Est2 ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
 Hs TCP1 ...RATSYVQCQGIPQGSILSTLLCSLCYG...
 consensus G QG S

Motif C
 Ep p123 ...PNVNLLMRLTDDYLLITTQENN...
 Sp Tez1 ...KKGSVLLRVVDDFLFITVNKKD...
 Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...
 Hs TCP1 ...RRDGLLLRLVDDFLLVTPHLTH...
 consensus DD L

Motif D
 Ep p123 ...NVSRENGFKFNMKKL...
 Sp Tez1 ...LNLSLRGFEEKHNFST...
 Sc Est2 ...KKLAMGGFQKYNKA...
 Hs TCP1 ...LRTLVRGVPEYGCVV...
 consensus G

FIGURE 49

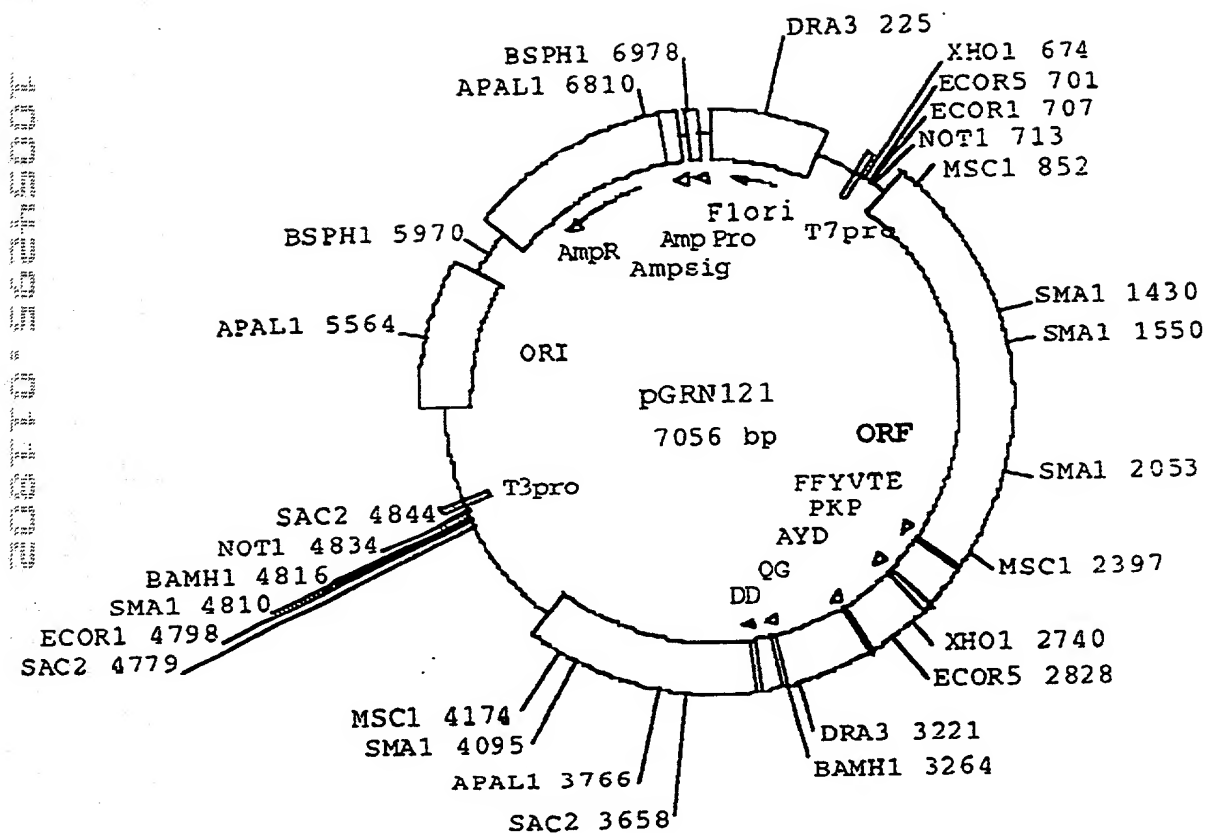


FIGURE 50

1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
 51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
 101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GCGCCTGGG
 151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCGCG
 201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGAN GN ANGGCNGCCC
 251 CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
 301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT
 351 TCGGCTTCGC GCTGCTGGAC GGGGCCCCGCG GGGGCCCCCG CGAGGCCTTC
 401 ACCACCAGCG TGCAGCTA CCTGCCAAC ACGGTGACCG ACGCACTGCG
 451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC
 501 TGGTTCACCT GCTGGCACGC TGC GCGNTNT TTGTGCTGGT GGNTCCACG
 551 TGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC
 601 TCAGGCCCGG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC
 651 CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
 701 CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC
 751 GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
 801 CCGTTGGGCA GGGGTCTGG GCCACCCGG GCAGGACGCC TGGACCGAGT
 851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
 901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG
 951 GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT
 1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCCTCTAC
 1051 TCCTCAGGCG ACAAGNACAC TGCGNCCCTC CTTCCTACTC AATATATCTG
 1101 AGGCCCAGCC TGA CTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG
 1151 TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA
 1201 GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAAACCAG
 1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
 1301 GCGGTACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
 1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG
 1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
 1451 CTGCTGCGC CGGCTGGTGC CCCAGGCCT CTGGGGCTCC AGGCACAACG
 1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
 1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG
 1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
 1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
 1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
 1751 GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT
 1801 TGCAAAGCAT TGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
 1851 CTGTCGGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
 1901 GACGTCCAGA CTCCGTTCA TCCCAAGCC TGACGGGCTG CGGCCGATTG
 1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG
 2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTACGCG TGCTCAACTA
 2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
 2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG
 2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
 2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA
 2251 AACCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC

FIGURE 50 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
 2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
 2401 GCCCCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
 2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC
 2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG
 2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG
 2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGC GTTTGGT
 2651 GGATGATTTT TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC
 2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG
 2751 CGGAAGACAG TGGTGAACCT CCCTGTAGAA GACGAGGCC TGGGTGGCAC
 2801 GGCTTTTGT CAGATGCCGG CCCACGGCCT ATTCCCCTGG TGC GGCCTGC
 2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC
 2901 CGGACCTCCA TCAGAGCCAG TCTCACCTT AACC GCGGCT TCAAGGCTGG
 2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGT CACA
 3001 GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC
 3051 ATCTACAAGA TCCTCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT
 3101 GCAGCTCCCA TTTCATCAGC AAGTTTGGAA GAACCC CACA TTTTCTCTGC
 3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG
 3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC
 3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC
 3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG
 3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC
 3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT
 3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC
 3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC CCAGGCCCGC
 3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT
 3601 CCGGCTGAAG GCTGAGTGT CCGCTGAGGC CTGAGCGAGT GTCCAGCCAA
 3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG
 3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCT CACCAGGAGC CCGGCTTCCA
 3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC
 3801 GCCCTGCCCT CCTTTGCCCT CCACCC CAC CATCCAGGTG GAGACCCTGA
 3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG
 3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT
 3951 GGGGGGAGGT GCTGTGGGAG TAAATACTG AATATATGAG TTTTTCAGTT
 4001 TTGAAAAAAAA AAAAAAAAAA AAAAAAAAAA

[illegible]

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Year	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

a	a	a	a	a	a
b	b	b	b	b	b
c	c	c	c	c	c

[illegible]

A P L A N A A P V S G A A W E P R A V F
R Y W Q M R F L F L E L L G N H A Q C F
P T G K C G P C F W S C L G T T R S A F

[illegible]

1261 1320

A L R G V P Q D A L F A A S C G H F S S R -
 D Y G V F L K T H C P L R A A V T P A A G -
 C T G C S S R R T A R C E L R S P Q Q P V -

[illegible]

A C L C P G E A P G I C G G P R G G G I U
 B V C A K E K P Q G S V A A P E E E E H R
 C S V P G R S P R A I W R P F R R R N T D

-----+-----+-----+-----+-----+-----+-----+-----+-----
1381 TGGGGGCGCCGCCACCTGCAGCAGGCGGTGCTGTGTCGACCAACGTTCCACATGCGGA 1440

a T F V A W C S C S A S T T A A P G R C T A -
b P P S P G A A A P P A Q Q P L A G V R L -
c P R R L V O L L R Q H S S P W Q V Y G F -

1441 -----+-----+-----+-----+-----+-----+-----+ 1500
ATGACGCGCCCGGACGGAACCGGCGGACCAACGGGGTTCGAGACCCCGAGGTTCGATGTTC

S C G P A C A G W C P Q A S G A F G I I
 R A G L P A P A G A P R P L G I Q A Q R
 V R A C L R R L V P P C L W G S R H N E

1501 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1560
TTTCGCGGAAGGAGTCTTGTGGTTCTTCACTAGAGGACCCCCCTCGTACGGTTTCGAGA

N A A S S G T P R S S S S P W G S M P S S
 T P L P Q E H Q E V H L P G E A C Q A L
 R R F L R N T K K F I S L G K H A K L S

1561 -----+-----+-----+-----+-----**1620**

-SCGAAGTCTCCTGCACTGCCACTTTCTATACGGCACGCCTGTGACCGSAAACCGAAGCGSTCCCTGG-

3 R C R S * R G R * A C G T A L C C A G A
b A A G A D V E D E R A G L R L A A Q E P
c L Q E L T W K M S V R D C A W L R E S P

1521 -----+-----+-----+-----+----- 1580
GTCCCCACCGACACAAGGCGGGGTCTCTGTTGGCAGACGCACCTCTCTTAGGACCGGTTCA

Q G L A V F R P Q S T V C V R E S W T S
R G W L C S C R R A T S A * G D P G Q V
G V G C V F A A E H F L R E E I L A K *

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: control group and experimental group. The control group was exposed to the control condition, while the experimental group was exposed to the experimental condition. The control condition consisted of a baseline measurement followed by a 10-minute rest period, while the experimental condition consisted of a baseline measurement followed by a 10-minute rest period and a 10-minute exposure to the experimental condition. The subjects were then asked to perform a task, and their performance was recorded. The results showed that the experimental group performed significantly better than the control group.

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b
c

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Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

T I S T G P G A P S C C V C G F R T R R -
 R Y F Q G L A H L R A A C A G P G P A A -
 D I H S A W R T F V L R V R A Q D F F P -

1. S C T L S R W M * R A R T T P S F R T -
 * A V L C Q G G C D G R V R H H P P G Q
 E L Y F V K V D V T G A Y D T I P O D K

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A      G S R R S S P A S S N P R T R T A C V G -
B      A H G G H R Q H H Q T P E H V L R A S V -
C      L T E V I A S I I K P Q N T Y C V R R Y

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a M P W S R R P P M G T S A R P S R A T S -
b C R G P E C R P W A R P Q G L Q E F R L -
c A V V Q K A A H G H V R K A F K S H V S

L P * Q T S S R T C D S S W L T C R ? T -
Y L D R P P A V H A T V R G S P A G ? Q -
T L T D L Q P Y M R O F V A H L Q ? N S

A R * G M P S S S S R A P P * M R P A V
 P A E G C R R H R A E L L P E * G Q Q W
 P L R D A V V I E O S S S L N E A S S G

A S S T S S Y A S C A T T P C A S G A S
P L R R L P T L H V P P R R A H Q G O V
L F D V F L R F M C H H A V R I R G K S

[illegible]

A T T P A M F G P P S E P V S P S T A A -
 b R L L Q L C F D L H Q S Q S H L Q P R L -
 c D Y S S Y A R T S I R A S L T F N R G F -

247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700
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[illegible]

FIGURE 51 (cont.)

GTGGGAAGCTCCCGGAGAGAGCTGACTGCGCTGGAGGCGCGCAGCCACCCGACCTGCT
 3361 -----+-----+-----+-----+----- 3420
 CAGGCTTCGAGGCGCGCTGCTGCGACTGACGGGACCTCCCGCTCGCTTGGCCGIGACG

 A V G S S R G R R * I F W R P Q F T R H C -
 B S E A P G D D A D C P G G R S Q P G T A -
 C R K L P G T T L T A L E A A A N P A L P -

 CCTCAGACITCAAGACCAATCTTGACTGATGGCCACCCGCCACAGCCAGGCGAGAGCA
 3421 -----+-----+-----+-----+----- 3480
 GGAGTCTGAAGTCTCTGGTAGGACCTGACTACCGGTGGCGGGTGTCTGGTCCCGCTCTCT

 A P Q T S E P S W T D G H P F T A R P R A -
 B L R L Q D H P G L M A T E P Q P G R E Q -
 C S D F K T I L D * W P F A H S Q A E S R -

 GACACCAGCAGCCCTCTCAAGCGGGCTCTACGTCCAGGGAGGGAGGGCGGCCACAC
 3481 -----+-----+-----+-----+----- 3540
 CTGTGCTGTCGGGACAGTCCCGGCCGAGATGCAGGGTCCCTCCCTCCCGCGGGTGTG

 A D T S S P V T P G S T S Q G G R G G P H -
 B T P A A L S R R A L R P R E G G A A H T -
 C H Q Q P C H A G L Y V P G R E G R P T P -

 CCAGGCCCGCACCGCTCGGAGCTCTCAAGGCTGAGTGAATGTTTGGCGAGGCGCTGCATGT
 3541 -----+-----+-----+-----+----- 3600
 GGTCGCGGCGTGGCGACCTCTCAGACTCGGACTCACTCACAACCGGCTCCGGACGTACA

 A P G P H R W E S E A * V S V W P R P A C -
 B Q A R T A G S L R P E * V P G R G L H V -
 C R P A P L G V * G L S E C L A E A C M S -

 CCGGCTGAAGCTGAGTGTTCGGCTGAGGCCCTGAGCTGCTCCAGCCAGCGCTGAGTCT
 3601 -----+-----+-----+-----+----- 3660
 GGGCGACTTCCGACTCACAAGCGGACTCCGGACTCGCTCAGAGTGGTTCGGACTCAG

 A P A E G * V S G * G L S E C P A K C * V -
 B R L F A E C P A E A * A S V Q P R A E C -
 C G * R L S V R L R P E R V S S Q G L S V -

 TTCAGTACACCTGCGCTCTTCACTTCCCCACAGGCTGGCGCTGGCTCCAGCCAGGGCT
 3661 -----+-----+-----+-----+----- 3720
 AGGTCTGTGTGACGGCAGAGCTGAACCGCTGTCCGACCGGAGCCGAGGTGGGCTCCCG

 A S S T P A V F T S P Q A G A R L H P R A -
 B P A H L P S S L P H R L A L G S T P G P -
 C Q H T C R L H F P T G W R S A P P Q G Q -

 AGCTTTTCTCACCAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCGAGA
 3721 -----+-----+-----+-----+----- 3780
 TCGAAAGGAGTGGTCTCGGCGCGAAGGTGAGGGTGTATCTTATCAGCTACCGGTCT

 A S F S S P G A R L P L P T * E * S T P E
 B A P P H Q E P G F H S P H R N S P S P D -
 C L F L T R S P A S T P H I G I V H F Q T -

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Year	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

A F A I V H F S P C P P L P S T P T I Q V -
 B S E L F T P R P A L L C L P F F F S R W -
 C F H C S P L A L P S F A F H P H H F G G -

A F T L E R T L G A L G I W S D Q R C A L -
 B F F * E G P W E L W E F G V T K G V P C -
 C D P E E D T G S S C N L E * P K V C P V

A Y T G E D P A P G W G S L W V K L G G C -
B T Q A R T L H L D G G P C G S N W G E V -
C H R R Q P C T W M C V P V G O I G G E C

A V G V K Y * I Y E F F S F E K K K K K
L W E * N T E Y M S F S V L K K K K K K
C G S K I L N I * V F Q P * K K K K K K -

а	к к к	-
б	к к	-
с	к к	-

FIGURE 52

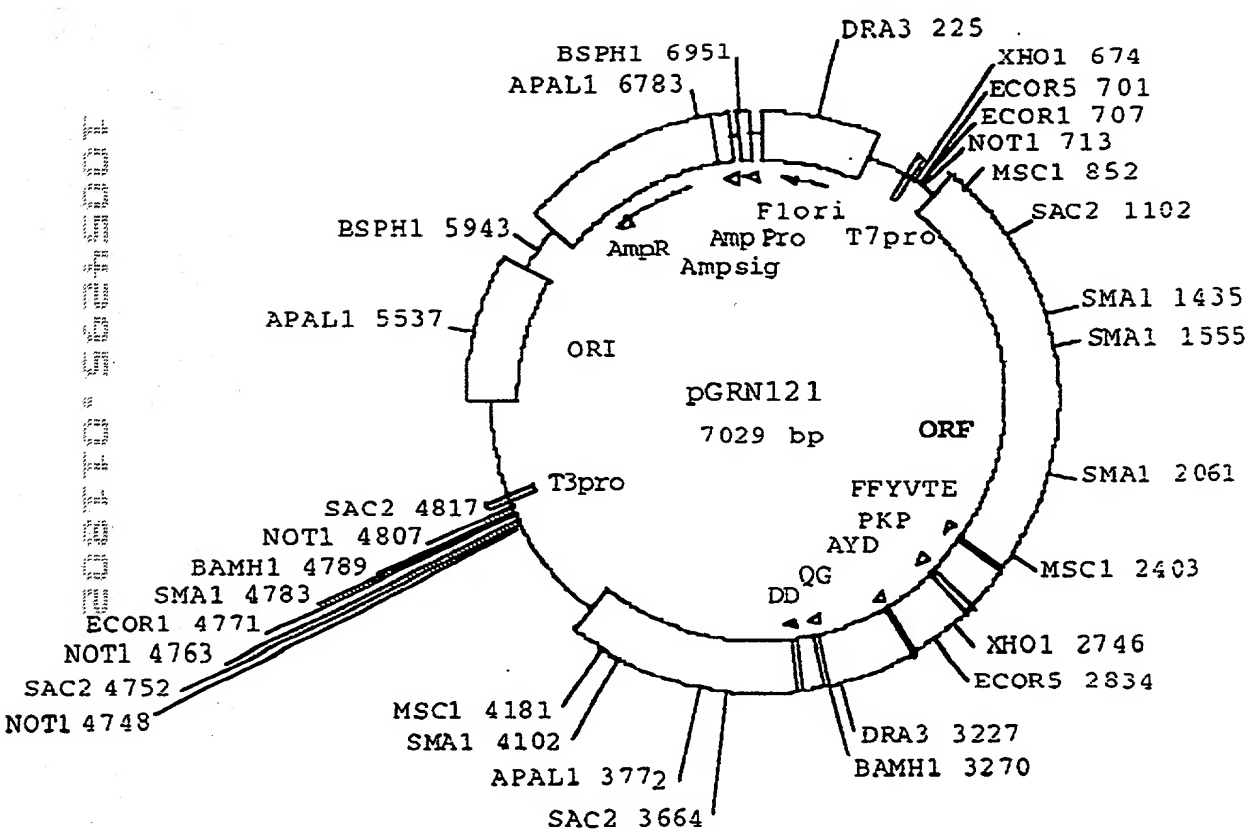


FIGURE 53

1
 met
 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG
 10
 pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC
 20 30
 his tyr arg glu val leu pro leu ala thr phe val arg arg leu
 CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG
 40
 gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
 GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT
 50 60
 phe arg ala leu val ala gln cys leu val cys val pro trp asp
 TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC
 70
 ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
 GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC
 80 90
 leu lys glu leu val ala arg val leu gln arg leu cys glu arg
 CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC
 100
 gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
 GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG
 110 120
 ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
 GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC
 ↑
 130
 tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
 TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

FIGURE 53 (cont.)

			140										150		
trp	gly	leu	leu	leu	arg	arg	val	gly	asp	asp	val	leu	val	his	
TGG	GGG	CTG	CTG	CTG	CGC	CGC	GTG	GGC	GAC	GAC	GTG	CTG	GTT	CAC	
								160							
leu	leu	ala	arg	cys	ala	leu	phe	val	leu	val	ala	pro	ser	cys	
CTG	CTG	GCA	CGC	TGC	GCG	CTC	TTT	GTG	CTG	GTG	GCT	CCC	AGC	TGC	
			170										180		
ala	tyr	gln	val	cys	gly	pro	pro	leu	tyr	gln	leu	gly	ala	ala	
GCC	TAC	CAG	GTG	TGC	GGG	CCG	CCG	CTG	TAC	CAG	CTC	GGC	GCT	GCC	
								190							
thr	gln	ala	arg	pro	pro	pro	his	ala	ser	gly	pro	arg	arg	arg	
ACT	CAG	GCC	CGG	CCC	CCG	CCA	CAC	GCT	AGT	GGA	CCC	CGA	AGG	CGT	
			200										210		
leu	gly	cys	glu	arg	ala	trp	asn	his	ser	val	arg	glu	ala	gly	
CTG	GGA	TGC	GAA	CGG	GCC	TGG	AAC	CAT	AGC	GTC	AGG	GAG	GCC	GGG	
								220							
val	pro	leu	gly	leu	pro	ala	pro	gly	ala	arg	arg	arg	gly	gly	
GTC	CCC	CTG	GGC	CTG	CCA	GCC	CCG	GGT	GCG	AGG	AGG	CGC	GGG	GGC	
			230										240		
ser	ala	ser	arg	ser	leu	pro	leu	pro	lys	arg	pro	arg	arg	gly	
AGT	GCC	AGC	CGA	AGT	CTG	CCG	TTG	CCC	AAG	AGG	CCC	AGG	CGT	GGC	
								250							
ala	ala	pro	glu	pro	glu	arg	thr	pro	val	gly	gln	gly	ser	trp	
GCT	GCC	CCT	GAG	CCG	GAG	CGG	ACG	CCC	GTT	GGG	CAG	GGG	TCC	TGG	
			260										270		
ala	his	pro	gly	arg	thr	arg	gly	pro	ser	asp	arg	gly	phe	cys	
GCC	CAC	CCG	GGC	AGG	ACG	CGT	GGA	CCG	AGT	GAC	CGT	GGT	TTC	TGT	
								280							
val	val	ser	pro	ala	arg	pro	ala	glu	glu	ala	thr	ser	leu	glu	
GTG	GTG	TCA	CCT	GCC	AGA	CCC	GCC	GAA	GAA	GCC	ACC	TCT	TTG	GAG	

FIGURE 53 (cont.)

290 300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

FIGURE 53 (cont.)

													440					450
ala	pro	glu	glu	glu	asp	thr	asp	pro	arg	arg	leu	val	gln	leu				
GCC	CCC	GAG	GAG	GAG	GAC	ACA	GAC	CCC	CGT	CGC	CTG	GTG	CAG	CTG				
													460					
leu	arg	gln	his	ser	ser	pro	trp	gln	val	tyr	gly	phe	val	arg				
CTC	CGC	CAG	CAC	AGC	AGC	CCC	TGG	CAG	GTG	TAC	GGC	TTC	GTG	CGG				
													470			480		
ala	cys	leu	arg	arg	leu	val	pro	pro	gly	leu	trp	gly	ser	arg				
GCC	TGC	CTG	CGC	CGG	CTG	GTG	CCC	CCA	GGC	CTC	TGG	GGC	TCC	AGG				
													490					
his	asn	glu	arg	arg	phe	leu	arg	asn	thr	lys	lys	phe	ile	ser				
CAC	AAC	GAA	CGC	CGC	TTC	CTC	AGG	AAC	ACC	AAG	AAG	TTC	ATC	TCC				
													500			510		
leu	gly	lys	his	ala	lys	leu	ser	leu	gln	glu	leu	thr	trp	lys				
CTG	GGG	AAG	CAT	GCC	AAG	CTC	TCG	CTG	CAG	GAG	CTG	ACG	TGG	AAG				
													520					
met	ser	val	arg	asp	cys	ala	trp	leu	arg	arg	ser	pro	gly	val				
ATG	AGC	GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT				
													530			540		
gly	cys	val	pro	ala	ala	glu	his	arg	leu	arg	glu	glu	ile	leu				
GGC	TGT	GTT	CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG				
													550					
ala	lys	phe	leu	his	trp	leu	met	ser	val	tyr	val	val	glu	leu				
GCC	AAG	TTC	CTG	CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG				
													560			570		
leu	arg	ser	phe	phe	tyr	val	thr	glu	thr	thr	phe	gln	lys	asn				
CTC	AGG	TCT	TTC	TTT	TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC				
													580					
arg	leu	phe	phe	tyr	arg	pro	ser	val	trp	ser	lys	leu	gln	ser				
AGG	CTC	TTT	TTC	TAC	CGG	CCG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC				
													590			600		
ile	gly	ile	arg	gln	his	leu	lys	arg	val	gln	leu	arg	glu	leu				
ATT	GGA	ATC	AGA	CAG	CAC	TTG	AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG				

FIGURE 53 (cont.)

610														
ser	glu	ala	glu	val	arg	gln	his	arg	glu	ala	arg	pro	ala	leu
TCG	GAA	GCA	GAG	GTC	AGG	CAG	CAT	CGG	GAA	GCC	AGG	CCC	GCC	CTG
620														
leu	thr	ser	arg	leu	arg	phe	ile	pro	lys	pro	asp	gly	leu	arg
CTG	ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	AAG	CCT	GAC	GGG	CTG	CGG
630														
640														
pro	ile	val	asn	met	asp	tyr	val	val	gly	ala	arg	thr	phe	arg
CCG	ATT	GTG	AAC	ATG	GAC	TAC	GTC	GTG	GGA	GCC	AGA	ACG	TTC	CGC
650														
660														
arg	glu	lys	arg	ala	glu	arg	leu	thr	ser	arg	val	lys	ala	leu
AGA	GAA	AAG	AGG	GCC	GAG	CGT	CTC	ACC	TCG	AGG	GTG	AAG	GCA	CTG
670														
phe	ser	val	leu	asn	tyr	glu	arg	ala	arg	arg	pro	gly	leu	leu
TTC	AGC	GTG	CTC	AAC	TAC	GAG	CGG	GCG	CGG	CGC	CCC	GGC	CTC	CTG
680														
690														
gly	ala	ser	val	leu	gly	leu	asp	asp	ile	his	arg	ala	trp	arg
GGC	GCC	TCT	GTG	CTG	GGC	CTG	GAC	GAT	ATC	CAC	AGG	GCC	TGG	CGC
700														
thr	phe	val	leu	arg	val	arg	ala	gln	asp	pro	pro	pro	glu	leu
ACC	TTC	GTG	CTG	CGT	GTG	CGG	GCC	CAG	GAC	CCG	CCG	CCT	GAG	CTG
710														
720														
tyr	phe	val	lys	val	asp	val	thr	gly	ala	tyr	asp	thr	ile	pro
TAC	TTT	GTC	AAG	GTG	GAT	GTG	ACG	GGC	GCG	TAC	GAC	ACC	ATC	CCC
730														
gln	asp	arg	leu	thr	glu	val	ile	ala	ser	ile	ile	lys	pro	gln
CAG	GAC	AGG	CTC	ACG	GAG	GTC	ATC	GCC	AGC	ATC	ATC	AAA	CCC	CAG
740														
750														
asn	thr	tyr	cys	val	arg	arg	tyr	ala	val	val	gln	lys	ala	ala
AAC	ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC	CAG	AAG	GCC	GCC
760														
his	gly	his	val	arg	lys	ala	phe	lys	ser	his	val	ser	thr	leu
CAT	GGG	CAC	GTC	CGC	AAG	GCC	TTC	AAG	AGC	CAC	GTC	TCT	ACC	TTG

FIGURE 53 (cont.)

			770										780		
thr	asp	leu	gln	pro	tyr	met	arg	gln	phe	val	ala	his	leu	gln	
ACA	GAC	CTC	CAG	CCG	TAC	ATG	CGA	CAG	TTC	GTG	GCT	CAC	CTG	CAG	
								790							
glu	thr	ser	pro	leu	arg	asp	ala	val	val	ile	glu	gln	ser	ser	
GAG	ACC	AGC	CCG	CTG	AGG	GAT	GCC	GTC	GTC	ATC	GAG	CAG	AGC	TCC	
			800										810		
ser	leu	asn	glu	ala	ser	ser	gly	leu	phe	asp	val	phe	leu	arg	
TCC	CTG	AAT	GAG	GCC	AGC	AGT	GGC	CTC	TTC	GAC	GTC	TTC	CTA	CCG	
								820							
phe	met	cys	his	his	ala	val	arg	ile	arg	gly	lys	ser	tyr	val	
TTC	ATG	TGC	CAC	CAC	GCC	GTG	CGC	ATC	AGG	GGC	AAG	TCC	TAC	GTC	
			830										840		
gln	cys	gln	gly	ile	pro	gln	gly	ser	ile	leu	ser	thr	leu	leu	
CAG	TGC	CAG	GGG	ATC	CCG	CAG	GGC	TCC	ATC	CTC	TCC	ACG	CTG	CTC	
								850							
cys	ser	leu	cys	tyr	gly	asp	met	glu	asn	lys	leu	phe	ala	gly	
TGC	AGC	CTG	TGC	TAC	GGC	GAC	ATG	GAG	AAC	AAG	CTG	TTT	GCG	GGG	
			860										870		
ile	arg	arg	asp	gly	leu	leu	leu	arg	leu	val	asp	asp	phe	leu	
ATT	CGG	CGG	GAC	GGG	CTG	CTC	CTG	CGT	TTG	GTG	GAT	GAT	TTC	TTG	
								880							
leu	val	thr	pro	his	leu	thr	his	ala	lys	thr	phe	leu	arg	thr	
TTG	GTG	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	ACC	TTC	CTC	AGG	ACC	
			890										900		
leu	val	arg	gly	val	pro	glu	tyr	gly	cys	val	val	asn	leu	arg	
CTG	GTC	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	GTG	AAC	TTG	CGG	
								910							
lys	thr	val	val	asn	phe	pro	val	glu	asp	glu	ala	leu	gly	gly	
AAG	ACA	GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC	CTG	GGT	GGC	
			920										930		
thr	ala	phe	val	gln	met	pro	ala	his	gly	leu	phe	pro	trp	cys	
ACG	GCT	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC	CCC	TGG	TGC	

FIGURE 53 (cont.)

940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

960
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

970
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

980
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

990
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1000
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1010
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1020
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1030
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1040
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

1050
1060
1070
1080
1090

FIGURE 53 (cont.)

1100 1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

1130 1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCCACAGCCAGGCCGAGAGCAGA
CACCAGCAGCCCTGTACGCCCCGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCACACCC
AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC
GGCTGAAGGCTGAGTGTCGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTC
CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG
CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT
CGCCATTGTTACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA
GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA
CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC
TGTGGGACTAAAATACTGAATATATGAGTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

FIGURE 54

KPN1 17050
KPN1 18560
ECOR1 19475
SAC1 19652
SAC1 21083
ECOR1 23539
SAC1 24607
SAC1 29043

<-TCP